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OM protein - protein search, using sw model	
Run on: November 3, 2005, 21:37:29 ; Search time 52.7808 Seconds (without alignments)	(without alignments)
Maximum cell updates/sec: 291.060	
Title: 09782816-1-22	32
Perfect score: 138	51
Sequence: 1 EVEKITKTVKESATEEKLTPIV <u>LAKOQAL</u> 30	33
Scoring table: BLOSUM62	34
Gappen 10.0 , Gapext. 0.5	35
Searched: 1612378 seqs, 512079187 residues	36
Total number of hits satisfying chosen parameters: 1612378	51
Minimum DB seq length: 0	37
Maximum DB seq length: 200000000	37.0
Post-processing: Minimum Match 0% DT	37.0
Maximum Match 100% DT	40
listing first 45 summaries DE	41
Database : UniProt-03; *	42
1: uniprot_sprot: *	43
2: uniprot_trembl: *	44
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	45
SUMMARIES	50.5
Result No.   Score   Query %   Match Length DB ID   Description	36.6
1   138   100.0   400   1 DCT2_HUMAN   013361 homo sapien	38.0
2   135   97.8   401   1 DCT2_MOUSE   Q99J88 mus musculus	39.0
3   135   97.8   402   2 Q6AVHS rattus norvegicus	39.5
4   114   82.6   338   07ZXY2 xenopus laevis	40.0
5   114   82.6   403   2 Q61RB3 xenopus laevis	41.0
6   109   79.0   403   2 Q66J30 xenopus laevis	42.0
7   109   79.0   405   2 Q7T3H1 brachydanio rerio	43.0
8   89   64.5   402   2 Q9PTG6 gallus gallus	44.0
9   56   40.6   333   2 Q874E7 paecilomyces thermophilus	45.0
10   54   39.1   445   2 Q72JL4 arabidopsis thaliana	46.0
11   54   39.1   500   1 C72Y_ARATH arabidopsis thaliana	47.0
12   54   39.1   769   Q6BP33 datura stramonium	48.0
13   54   933   1 Q6AZBR glandularia azorica	49.0
14   53   38.4   416   2 Q6BFZ2 paramecium tetraurelia	50.0
15   53   38.4   710   2 Q6CF32 yarrowia lipolytica	51.0
16   53   38.4   757   2 Q75C25 aspergillus gossypii	52.0
17   53   38.4   1373   2 Q01787 cantharidus haemactis	53.0
18   52   37.7   449   2 Q738U0 bacillus cereus	54.0
19   52   37.7   452   2 Q81DX2 bacillus ce	55.0
20   52   37.7   470   2 Q6FAP3 acinetobacter	56.0
21   52   37.7   1430   2 Q7RT55 plasmidium	57.0
22   51   37.0   131   2 Q8TZ25 pyrococcus	58.0
23   51   37.0   180   2 Q25336 parechymus	59.0
24   51   37.0   319   2 Q8P418 methanococcus	60.0
25   51   37.0   378   2 Q6UYC7 actinomycet	61.0
26   51   37.0   389   2 Q8KHB8 helicobacte	62.0
27   51   37.0   389   2 Q8LON4 helicobacte	63.0
28   51   37.0   389   2 Q8LON6 helicobacte	64.0
29   51   37.0   389   2 Q8LON9 helicobacte	65.0
30   51   37.0   389   2 Q8LPO0 helicobacte	66.0
31   51   37.0   389   2 Q8LPO1 helicobacte	67.0

RC TISSUE=Platelet; PubMed=12665801; DOI=10.1038/nbt810;  
 RX MEDLINE=22608398; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,  
 RA Thomas G.R., Vandekerckhove J.;  
 RT "Exploring proteomes and analyzing protein processing by mass  
 RT spectrometric identification of sorted N-terminal peptides.";  
 RL Biotechnol. 21: 566-569(2003).  
 CC -!- FUNCTION: Modulates cytoplasmic dynein binding to an organelle,  
 CC and plays a role in prometaphase chromosome alignment and spindle  
 CC organization during mitosis. May play a role in synapse formation  
 CC during brain development.  
 CC -!- SUBUNIT: Subunit of dynein, a multiprotein complex associated  
 CC with dynein.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.  
 CC  
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 CC or send an email to license@isb-sib.ch).  
 CC  
 DR EMBL; U50733; AAC50423.1; -.  
 DR BC001718; AAH0718.1; -.  
 DR BC009468; AAH09468.1; -.  
 DR EMBL; BC014083; AAH14083.1; -.  
 DR EMBL; AY189155; AA034395.1; -.  
 DR Genew; HNCN:2112; DCTN2.  
 DR MMDB; 607176; -.  
 DR GO; GO:0005813; C:centrosome; TAS.  
 DR GO; GO:000569; C:dynein complex; TAS.  
 DR GO; GO:0000776; C:kinetochore; TAS.  
 DR GO; GO:0008283; P:cell proliferation; TAS.  
 DR GO; GO:007067; :mitosis; TAS.  
 DR InterPro; IPR06996; Dynamin.  
 DR Pfam; PF04912; Dynamin: 1.  
 KW Coiled coil; Cytoskeleton; Direct protein sequencing; Dynein;  
 KW Membrane; Microtubule; Motor protein.  
 FT INIT\_MET 0  
 FT DOMAIN 98 131 Coiled coil (Potential).  
 FT DOMAIN 213 243 Coiled coil (Potential).  
 FT DOMAIN 378 398 Coiled coil (Potential).  
 FT CONFLICT 34 34 A -> AFAQE (in Ref. 1).  
 FT CONFLICT 35 35 E -> ELE (in Ref. 3).  
 FT SEQUENCE 381 384 LATV -> PGHS (in Ref. 3).  
 SQ 400 AA; 44099 MW; 0A95AE95C0BB270F CRC64;  
 Query Match 100.0%; Score 138; DB 1; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-09;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 EVEKIKITIVKESATEBKLTPLVILAKOAL 30  
 Db 115 EVEKIKITIVKESATEBKLTPLVILAKOAL 144  
 RESULT 2  
 DCT2\_MOUSE STANDARD PRT; 401 AA.  
 ID DCT2\_MOUSE  
 AC Q99KU8;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DR Dynactin complex 50 kDa subunit (50 kDa dynein-associated polypeptide)  
 DE (p50 dynamin) (DCTN-50) (Dynactin 2) (Growth cone membrane protein  
 DE 23-48K) (GMP23-48K).  
 GN Name=Dctn2;  
 OS Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
 OC NCBI\_TaxID=10990;  
 RN [1]

RQ SEQUENCE FROM N.A.  
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.D., Feingold E.A., Grouse L.H., Dege J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shannen C.M., Schuler G.D.,  
 RA Altchul S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Bhattacharyya N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Matsubara K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Lockettano N.A., Peters G.J., Abramson R.D., Mallory S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Heaton E., Kettemann M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., couchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzwicki J., Skalnik U., Smallius D.B.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RR SEQUENCE OF 65-74; 77-91; 102-116; 156-170; 194-216 AND 309-320.  
 RR SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
 RR TISSUE=Brain;  
 RR INTERACTION WITH BICD2.  
 RX MEDLINE=21376052; PubMed=11483508; DOI=10.1093/embj/20.15.4041;  
 RA Hoogenraad C.C., Alkmanova A., Howell S.A., Doortland B.R.,  
 RA de Zeeuw C.I., Willemse R., Visser P., Grosveld F., Galjart N.;  
 RT "Mammalian Golgi-associated Bicaudal-D2 functions in the dynein-  
 RT dynein pathway by interacting with these complexes.";  
 RL EMBO J. 20:4041-4054 (2001).  
 CC -!- FUNCTION: Modulates cytoplasmic dynein binding to an organelle,  
 CC and plays a role in prometaphase chromosome alignment and spindle  
 CC organization during mitosis. May play a role in synapse formation  
 CC during brain development.  
 CC -!- SUBUNIT: Subunit of dynein, a multiprotein complex associated  
 CC with dynein (By similarity). Interacts with BICD2.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.  
 CC -!- DEVELOPMENTAL STAGE: Present at high levels in both cytoplasmic  
 CC and membrane-associated forms in neonates. Levels of membrane-  
 CC associated form are greatly reduced in the adult.  
 CC  
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 CC  
 DR EMBL; BC004613; AAH04613.1; -.  
 DR MGDB; MGI:107733; Dctn2.  
 DR InterPro; IPR06996; Dynamin.  
 DR Pfam; PF04912; Dynamin; 1.  
 KW Coiled coil; Cytoskeleton; Direct protein sequencing; Dynein;  
 KW Membrane; Microtubule; Motor protein.  
 FT INIT\_MET 0 By Similarity.  
 FT DOMAIN 98 131 Coiled coil (Potential).  
 FT DOMAIN 214 244 Coiled coil (Potential).  
 SQ SEQUENCE 401 AA; 43985 MW; 1535E4ABD5940BC CRC64;  
 Query Match 97.8%; Score 135; DB 1; Length 401;  
 Best Local Similarity 96.7%; Pred. No. 4.5e-09; 0; Indels 0; Gaps 0;





RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	RESULT 9	Q874E7	PRELIMINARY;	PRT;	333 AA.
RA	Fahy J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		Q874E7	ID		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		Q874E7	AC		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		Q874E7	DT	01-JUN-2003 (TREMblrel. 24, Created)	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		Q874E7	DT	01-JUN-2003 (TREMblrel. 24, Last sequence update)	
RA	Krzewinski M.I., Skalska U., Smailus D.E., Schneich A., Schein J.B.,		Q874E7	DT	01-JUN-2003 (TREMblrel. 24, Last annotation update)	
RA	Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human		MATI-1-2.	DE		
RT	RT and mouse cDNA sequences.",			GN	Name=MATI-1-2;	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			OS	Paecilomyces tenuipes.	
RN	[2]			OC	Bakteria; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;	
RP	SEQUENCE FROM N.A.			OC	Eurotiales; Trichocomaceae; Paecilomycetidae; Paecilomycetes.	
RC	TISSUE=Embryo;			OX	Bakteria; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;	
RA	Strausberg R.;			NCBI_TaxID=45847;		
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			RN		
DR				SEQUENCE FROM N.A.		
DR	EMBL; BC053120; AACR53120_1; -.			PubMed=15321663; DOI=10.1016/j.fembe.2004.06.033;		
DR	ZFBIN; ZDB-GENB-040426-1279; zgc:63867.			RA	Yokoyama E., Yamagishi K., Hara A.; "Development of a PCR-based mating-type assay for Clavicipitaceae.";	
DR	GO; GO:005869; C:dynein complex; IEA.			RT	FEMS Microbiol. Lett. 237:205-212(2004).	
DR	GO; GO:0007017; P:microtubule-based process; IEA.			RL	[2]	
DR	InterPro; IPR006396; Dynamitin.			RN	SEQUENCE FROM N.A.	
DR	Pfam; PF04912; Dynamitin; 1.			RP	MEDLINE=22783895; PubMed=12902305;	
SQ	SEQUENCE 405 AA; 44625 MW; CRC64;			RX	DOI=10.1128/AEM.68.8.5019-5022.2003;	
Db	118 DVKEIQTISKESGAERKTPVALLAQAOI 147			RA	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				RT	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				DR	EMBL; AB096216; BAC67940_1; -.	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
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				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
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				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
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				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
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				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
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				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
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				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
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				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
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				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
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				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
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				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
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				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
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				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
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				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 55904890716BBF6 CRC64;	
				RA	DOI=10.1128/AEM.68.8.5019-5022.2003;	
				RT	Yokoyama E., Yamagishi K., Hara A.; "Structures of the mating-type loci of Cordyceps takaonmontana.";	
				DR	Appl. Environ. Microbiol. 69:5019-5022(2003).	
				SQ	SEQUENCE 333 AA; 37756 MW; 5	



RESULT 13	
GLAND_AZOBR	STANDARD; PRT; 933 AA.
ID	PUBRD1; 10-OCT-2003 (Rel. 42, Created)
DT	10-OCT-2003 (Rel. 42, last sequence update)
DT	05-JUL-2004 (Rel. 44, last annotation update)
DE	[protein-PII] uridylyltransferase (EC 2.7.7.59) (PII uridylyl-transferase) (Uridyllyl removing enzyme) (UTase).
DE	Name=glnD;
OS	Azospirillum brasilense.
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC	Rhodospirillaceae; Azospirillum.
NCBI_TaxID	192;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Sp1 / ATCC 29145;
RA	Van Dommelen A., Keijers V., Somers E., Vanderleyden J.;
RT	"Cloning and characterization of the Azospirillum brasilense glnD gene and analysis of a glnD mutant.";
RT	Mol. Gen. Genet. 266:813-820(2002).
-1	FUNCTION: Modifies, by uridylylation or deuridylylation the PII (glnB) regulatory protein.
-1	CATALYTIC ACTIVITY: UTP + [protein-PII] = diphosphate + uridylyl-
-1	[protein-PII].
CC	-----
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
CC	-----
CC	EMBL; API49716; AAL87737.1; -.
DR	HAMAP; MF_000277; -; 1.
DR	InterPro; IPR02912; ACT.
DR	InterPro; IPR06674; HD hydro.
DR	InterPro; IPR03607; Met_phos hydro.
DR	InterPro; IPR02934; NTP_transf.
DR	InterPro; IPR010013; Uracil_glnD.
PFAM	PF01842; ACT; 2.
DR	PFAM; PF01666; HD; 1.
DR	PFAM; PR01909; NTP_transf_2; 1.
DR	SMART; SM00471; HOG; 1.
DR	TIGRFAMs; TIGR01633; Uracil_glnD; 1.
KW	Nitrogen fixation; Nucleotidyltransferase; Transferase.
SQ	SEQUENCE 933 AA; 104601 MW; 35569250411BB9E7 CRC64;
Query Match	39.1%; Score 54; DB 1; Length 933; Best Local Similarity 42.9%; Pred NO. 2.8e-02; Matches 12; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
Qy	3 EKIKTTVKESATEKLTIPVLAQKQAL 30
Ds	36 EDIETLVAHGTGDKRPAHLRGAL 63
RESULT 14	
O6BF22	PRELIMINARY; PRT; 416 AA.
ID	QBFB22; 25-OCT-2004 (TREMBREL; 28, Created)
DT	25-OCT-2004 (TREMBREL; 28, last sequence update)
DT	21-OCT-2004 (TREMBREL; 28, Last annotation update)
DE	Hypothetical protein.
OS	OrfNames=PTMB_23; Paramecium tetrauraria.
RESULT 15	
Q6CF32	PRELIMINARY; PRT; 710 AA.
ID	Q6CF32; 25-OCT-2004 (TREMBREL; 28, Created)
DT	25-OCT-2004 (TREMBREL; 28, last sequence update)
DT	25-OCT-2004 (TREMBREL; 28, last annotation update)
DE	Similarity (Fragment); ORFName=YAL10B06929;
GN	Yarrowia lipolytica CILB99.
OS	Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC	Saccharomyctales; Dibopascaceae; Yarrowia.
NCBI_TaxID	284591;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CLIB99;
RG	Genoliviers;
RA	Dujon B., Sherman D., Fischer G., Durrieus P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E., Goffard N., Franssen L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne C., Bleyleston C., Boisrame A., Boyer J., Catolicco L., Confaolioli F., de Darvaru A., Desponts L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemire M., Lesur I., Ma L., Muller H., Nicaud J.M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O., Peillen S., Potier S., Richard G.P., Straub M.L., Suleau A., Swennere D., Tekla F., Wesołowska-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpetti C., Gaillardin C., Weissenbach J., Wincker P., Soucet J.-L.;
RT	Genome evolution in yeasts. ";
RL	Nature 430:35-44(2004).
[2]	SEQUENCE FROM N.A.
RC	STRAIN=CLIB99;
RA	Genoscope;
RA	Submitted; (TUL-2004) to the EMBL/GenBank/DBJ databases.
RL	CR38228; CA362975.1; -.
DR	

DR InterPro; IPR005011; SART\_1.  
DR Pfam; PF03343; SART\_1; 1.  
FT NON\_TER  
SQ SEQUENCE 710 AA; 81568 MW; 89C3CA466BB2F69B CRC64;  
Query Match 38.4%; Score 53; DB 2; Length 710;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 12; Conservative 3; Mismatches 9; Indels 0; Gaps 0;  
QY 6 KITVVKESATEKKUTVLLAQAA 29  
Db 426 KNLMKSQRNPKLTPRQLAQAA 449  
Search completed: November 3, 2005, 22:03:01.  
Job time : 55.7808 secB

GenCore version 5.1.6  
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## OM protein - protein search, using BW model.

Run on: November 3, 2005, 21:32:33 ; Search time 71.1872 Seconds  
(without alignments)

282.516 Million cell updates/sec

Title: 09782816-51  
Perfect score: 251  
Sequence: 1 GVKETPQQKIQRLHIEWQEL.....ESATEERKLTPVLLAKOAL 52

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext: 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04; \*  
1: geneseq1980s; \*  
2: geneseq2000s; \*  
3: geneseq2001s; \*  
4: geneseq2002s; \*  
5: geneseq2003ab; \*  
6: geneseq2003ab; \*  
7: geneseq2004s; \*  
8: geneseq2004s; \*

**pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	251	100.0	314	8 ABM81421	Abm81421 Tumour-as
2	251	100.0	378	6 ABP98851	Abp98851 Human str
3	251	100.0	401	7 ADJ60563	Adj69563 Human hea
4	251	100.0	406	5 ABP50108	Abp50108 Human p50
5	251	100.0	465	3 ABP5968	Aab5968 Breast can
6	248	98.8	183	5 ABP5019	Abp5019 Mouse p50
7	246	98.5	52	5 ABP5016	Abp53016 Cellular
8	231	92.0	134	4 ABG75956	Aag75956 Human oJ
9	113	45.0	22	5 ABP52968	Abp52968 Cellular
10	107	42.6	21	5 ABP52969	Abp52969 Cellular
11	103	41.0	20	5 ABP52970	Abp52970 Cellular
12	103	41.0	23	5 ABP52966	Abp52966 Cellular
13	98	39.0	19	5 ABP52971	Abp52971 Cellular
14	93	37.1	18	5 ABP52972	Abp52972 Cellular
15	88	35.1	17	5 ABP52973	Abp52973 Cellular
16	81	32.3	16	5 ABP52974	Abp52974 Cellular
17	76	30.3	15	5 ABP52975	Abp52975 Cellular
18	72.5	28.9	53	5 ABP53017	Abp53017 Cellular
19	72.5	28.9	380	4 ABP5088	Abp59088 Drosophil
20	72.5	28.9	380	5 ABP5020	Abp53020 Drosophil
21	71	28.3	14	5 ABP52976	Abp52976 Cellular
22	70	27.9	1087	4 ABB65359	Abb65359 Drosophil
23	70	27.9	1087	4 ABB65358	Abb65358 Drosophil
24	68	27.1	2368	4 AAB34139	Aab34139 Staphyloc
25	68	27.1	2368	4 AAU36796	Aau36796 Staphyloc

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04; \*  
1: geneseq1980s; \*  
2: geneseq2000s; \*  
3: geneseq2001s; \*  
4: geneseq2002s; \*  
5: geneseq2003ab; \*  
6: geneseq2003ab; \*  
7: geneseq2004s; \*  
8: geneseq2004s; \*

## RESULT 1

ABMB1421  
ID ABMB1421 standard; protein; 314 AA.  
XX  
AC ABMB1421;  
XX  
DT 18-NOV-2004 (First entry)  
XX  
DE Tumour-associated antigenic target (TAT) polypeptide PRO82191, SEQ:3675.  
XX  
Tumour-associated antigenic target (TAT) polypeptide PRO82191, SEQ:3675.  
KW tumour; diagnosis; cell proliferative disorder; breast cancer; liver cancer;  
KW colorectal cancer; lung cancer; ovarian cancer; central nervous system cancer;  
KW cervical cancer; melanoma; leukaemia; hybridiostatic; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic.  
KW chromosomal aberration; chromosomal mapping; cytostatic; gene mapping; gene therapy; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO2004030615-A2.  
XX  
PD 15-APR-2004.  
XX  
PP 29-SEP-2003; 2003WO-US028547.  
XX  
PR 02-OCT-2002; 2002US-0414971P.  
XX  
PA (GENTHER ) GENENTECH INC.  
XX  
PT Wu TD, Zhang Z, Zhou Y;  
XX  
DR WPI; 2004-347921/32.  
DR N-ISDB; ACN39497.  
XX  
PT New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.  
XX  
PS Claim 12; SEQ ID NO 3675; 7273pp; English.  
XX  
CC The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and

Ada89551 Staphyloc  
Aau37374 Staphyloc  
Aau34320 Staphyloc  
Abt19020 Pathogen  
Abm71899 Staphyloc  
Abu15838 Protein e  
Abp62804 Methicillin  
Abp52977 Cellular  
Abu4043 Protein e  
Aay7731 Protein i  
Aam19875 Human Pro  
Ab28754 Rice PNI-  
Ad84304 Bacterial  
Aao12168 Human Pol  
Aag03725 Human sec  
Aaw64545 Human sto  
Abd10278 Human fet  
Aau12172 Human PRO  
Abd17616 Novel hum  
Abu80870 Human PRO

polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, nucleic acid-binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukemia. TAT nucleic acids may further be used as hybridisation probes in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention.

**Sequence 314 AA;**  
**SQ**

```

Query Match          100.0%;  Score 251;  DB 8;  Length 314;
Best Local Similarity 100.0%;  Pred. No. 6e-21;  Matches 52;  Conservative 52;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 52;  Conservative 52;  Mismatches 0;  Indels 0;  Gaps 0;
QY 1 GVKETPQQKYQRLIHEVQELTTEVKIKITVKESATEEKUTPVUJAKQLAL 52
Db 7 GVKETPQQKYQRLIHEVQELTTEVKIKITVKESATEEKUTPVUJAKQLAL 53

```

**RESULT 2**  
**ABP9851**  
**ID** ABP9851 standard; protein; 378 AA.  
**XX**  
**AC** ABP9851;  
**XX**  
**DT** 15-JUL-2003 (first entry)  
**XX**  
**DE** Human structural and cytoskeletal associated protein #42.  
**KW** Cytostatic; antiarteriosclerotic; anticonvulsant; nootropic; antianginal; neuroprotective; cerebroprotective; hypotensive; cardiotonic; osteopathic; antiinflammatory; antiarthritic; vincule; gene therapy; human; stroke; structural and cytoskeleton-associated protein; SCAP; cancer; angina; atherosclerosis; epilepsy; Huntington's disease; hypertension; heart failure; osteoporosis; osteoarthritis.  
**KW**  
**OS** Homo sapiens.  
**XX**  
**PN** WO2003031940-A2.  
**XX**  
**PD** 17-APR-2003.  
**XX**  
**PF** 10-OCT-2002; 2002W0-US032851.  
**PR** 12-OCT-2001; 2001US-0328931P.  
**PR** 19-OCT-2001; 2001US-0360681P.  
**PR** 02-NOV-2001; 2001US-0343896P.  
**PR** 03-NOV-2001; 2001US-0343308P.  
**PR** 16-NOV-2001; 2001US-0322385P.  
**PR** 07-DEC-2001; 2001US-034776P.  
**PR** 11-JAN-2002; 2002US-0347703P.  
**XX**  
**PA** (INCY-) INCYTE GENOMICS INC.  
**XX**  
**PI** Bachia NK, Blatia U, Blake JJ, Borowsky ML, Burrill JD, Chang H, Chawla NK, Elliott VS, Emerling BM, Forshey JU, Gorvard AE, Griffin JA, Hafalia AJA, Ho A, Ison CH, Kable AE, Khare R, Lal PG, Lee S, Lee EA, Lee SY, Lehr-Mason PM, Li JK, Lindquist EA, Luo W, Marquis JP, Ramkumar J, Richardson TW, Sprague WM, Swarnakar A, Tang YT, Warren BA, Yang J, Yue H, Zebrafadian Y, Zheng W;  
**PI** DR; WPI; 2003-403125/38.  
**XX**  
**PT** New human structural and cytoskeleton-associated proteins (SCAP) useful for diagnosing, treating and preventing diseases or conditions associated



CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the CC isolation and characterisation of the DNA and protein sequences of the CC invention. The breast and ovarian cancer associated DNA, protein, agonist CC or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; CC neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; CC antiinflammatory; antiulcer; anticonvulsant; antibacterial; antifungal; anti-parasitic and cardiotonic activity. The Polynucleotide and CC protein sequences are used in the diagnosis of cancer, particularly CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists CC and antagonists may also be used in the diagnosis, prevention and treatment CC of immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; CC cardiovascular diseases such as cerebral ischaemia; wound healing; CC infectious diseases

CC SQ Sequence 465 AA;

Query Match 100.0%; Score 251; DB 3; Length 465;  
Best local Similarity 100.0%; Pred. No. 9.4e-21; Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKEPQQKQYQRLLHEVQLTTEVEKIKITVKESATEEKLTIPVLLAKQAL 52  
Db 158 GVKEPQQKQYQRLLHEVQLTTEVEKIKITVKESATEEKLTIPVLLAKQAL 209

RESULT 6

ID ABP53019  
ID ABP53019 standard; protein; 183 AA.

AC XX

AC ABP53019;

XX DT 05-NOV-2002 (first entry)

XX DE Mouse p50 amino acid sequence SEQ ID NO:54.

XX DE

XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;

XX KW p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma;

XX KW sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;

XX KW glial disorder; astrocytial disorder; hypothalamic disorder; inflammatory;

XX KW glandular disorder; macrophagal disorder; epithelial disorder; inflammatory;

XX KW stromal disorder; blastocoelic disorder; angiogenic disorder;

XX KW immunologic disorder; immunologic disorder; angiogenic disorder;

XX OS XX

OS Mus musculus.

XX PN WO200264779-A2.

XX PD 22-AUG-2002.

XX PR 21-JAN-2002; 2002WO-US001708.

XX PA (REGC ) UNIV CALIFORNIA.

XX PT Sharp DJ, Rogers GC, Schooley JM;

XX DR WPI; 2002-657599/70.

XX PT New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemic and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.

XX PS Disclosure; Fig 2; 55pp; English.

CC The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2), Where (P1) and (P2) are the sequences given in ABP5266 and ABP5296<sup>7</sup> and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities

CC and can be used as p50/dynamitin inhibitors and in gene therapy. The CC peptides, nucleic acid molecules and methods from the present invention CC are useful for treating cancer by inhibiting cellular proliferation, such CC as benign or malignant tumours (renal, liver, kidney, bladder, breast, CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, head and CC neck tumours); leukaemias and lymphoid malignancies, other disorders such CC as neuronal, glial, astrocytal, hypothalamic and other glandular, CC macrophagal, epithelial, bromal, and blastocoelic disorders; and CC inflammatory, angiogenic and immunologic disorders. The present sequence CC represents mouse p50 which is given in the exemplification of the present invention.

XX SQ Sequence 183 AA;

Query Match 98.8%; Score 248; DB 5; Length 183;  
Best local Similarity 98.1%; Pred. No. 7.1e-21; Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKEPQQKQYQRLLHEVQLTTEVEKIKITVKESATEEKLTIPVLLAKQAL 52  
Db 94 GVKEPQQKQYQRLLHEVQLTTEVEKIKITVKESATEEKLTIPVLLAKQAL 145

RESULT 7

ID ABP53016  
ID ABP53016 standard; peptide; 52 AA.

AC XX

AC ABP53016;

XX DT 05-NOV-2002 (first entry)

XX DE Cellular proliferation peptide inhibitor SEQ ID NO:51.

XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; KW p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma;

XX KW sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;

XX KW stromal disorder; macrophagal disorder; epithelial disorder; inflammatory disorder.

XX OS Homo sapiens.

OS Mus musculus.

OS Synthetic.

XX OS

Key FH Location/Qualifiers  
FT Misc-difference 44  
FT /label= "Leu" Val  
FT /note= "Leu in humans and Val in Mus musculus"

XX PN WO200264779-A2.

XX PD 22-AUG-2002.

XX PR 21-JAN-2002; 2002WO-US001708.

XX PA (REGC ) UNIV CALIFORNIA.

XX PT Sharp DJ, Rogers GC, Schooley JM;

XX DR WPI; 2002-657599/70.

XX PT New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemic and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.

XX PS Claim 2; Page 31; 55pp; English.

CC The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2), Where (P1) and (P2) are the sequences given in ABP5266 and ABP5296<sup>7</sup> and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities

CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the  
 CC sequences given in ABP52966 and ABP52957 and can have C-terminal and N-  
 CC terminal extensions. (1) have cytostatic and antiinflammatory activities  
 CC and can be used as p50/dynamitin inhibitors and in gene therapy. The  
 CC peptides, nucleic acid molecules and methods from the present invention  
 are useful for treating cancer by inhibiting cellular proliferation, such  
 as benign or malignant tumours (renal, liver, kidney, bladder, breast,  
 CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid,  
 CC and neck tumours); leukaemias and lymphoid malignancies, and various head and  
 CC neck tumours; gliomas and other disorders such as neuronal, glial, astrocyt, hypothalamic and other glandular,  
 CC macrophagal, epithelial, stromal and blastocoeleic disorders; and  
 CC inflammatory, angiogenic and immunologic disorders. The present sequence  
 CC represents a specifically claimed peptide inhibitor of cellular  
 CC proliferation from the present invention

SQ Sequence 52 AA:

Query Match 98.0%; Score 246; DB 5; Length 52;  
 Best Local Similarity 98.1%; Pred. No. 2.8e-21; Mismatches 0; Indels 0; Gaps 0;  
 Matches 51; Conservative 0; Mi smatches 0; Indels 0; Gaps 0;

OQ 1 GVKETPQQKYQRLLHEVQELTTEVERKIKITVKESATEEKUTPVVLAKQAL 52  
 Db 1 GVKETPQQKYQRLLHEVQELTTEVERKIKITVKESATEEKUTPVVLAKQAL 52

RESULT 8

ID AGG75956 standard; protein; 134 AA.  
 XX AGG75956;  
 AC 03-SEP-2001 (first entry)  
 DT DE Human colon cancer antigen protein SEQ ID NO:6720.  
 DE Human colon cancer antigen protein SEQ ID NO:6720.  
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;  
 KW colorectal carcinoma; chromosome 12.  
 OS Homo sapiens.  
 XX WO200122920-A2.  
 XX PD 05-APR-2001.  
 XX PP 28-SEP-2000; 2000MO-US026524.  
 XX PR 29-SEP-1999; 99US-0157137P.  
 PR 03-NOV-1999; 99US-0163280P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PT Ruben SM, Barash SC, Birse CE, Rosen CA;  
 XX DR WPI; 2001-235357/24.  
 DR N-PSDB; AAH35361.

XX PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.

XX PS Claim 11; Page 8181; 9803pp; English.

XX DR WPI; 2001-235357/24.

XX PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.

XX PS Claim 11; Page 8181; 9803pp; English.

XX New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.

XX PS Claim 1; Page 29; 55pp; English.

XX The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP2966 and ABP52957 and can have C-terminal and N-terminal extensions. (1) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and

CC to produce the colon cancer-associated ps, by inserting the nucleic acids  
 CC into a host cell and culturing the cell to express the proteins. N and P  
 CC can be used in the prevention, diagnosis and treatment of colorectal  
 CC carcinomas and cancers. AAB7196 to AAB37204 and AAB77789 represent  
 CC sequences used in the exemplification of the present invention. N-B.  
 Pages 666 to 682 and page 7053 of the sequence listing were missing at  
 CC time of publication, meaning no sequences are present for SEQ ID NO:1027  
 CC to 1052, 7921 and 7922  
 XX Sequence 134 AA:  

Query Match 92.0%; Score 231; DB 4; Length 134;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-19;  
 Matches 48; Conservative 0; Mi smatches 0; Indels 0; Gaps 0;

OQ 5 TPOQKQRQLLHEVQELTTEVERKIKITVKESATEEKUTPVVLAKQAL 48  
 Db 1 TPOQKQRQLLHEVQELTTEVERKIKITVKESATEEKUTPVVLAKQAL 48

RESULT 9

ID ABP52968 standard; peptide; 22 AA.  
 XX ABP52968;  
 AC 05-NOV-2002 (first entry)  
 DT DE Cellular proliferation inhibitor related peptide SEQ ID NO:3.  
 XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;  
 KW p50 inhibitor; dynamitin inhibitor; gene therapy; tumor; carcinoma;  
 KW sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;  
 KW glial disorder; astrocytal disorder; hypothalamical disorder; inflammatory;  
 KW glandular disorder; macrophagal disorder; epithelial disorder;  
 KW stromal disorder; blastocoeleic disorder; angiogenic disorder;  
 KW immunologic disorder.  
 XX Homo sapiens.  
 OS Mus musculus.  
 OS Synthetic.  
 XX WO200264779-A2.  
 XX PD 22-AUG-2002.  
 XX PP 21-JAN-2002; 2002MO-US001708.  
 XX PR 14-FEB-2001; 2001US-00782816.  
 XX (REGC ) UNIV CALIFORNIA.  
 XX PI Sharp DJ, Rogers GC, Scholey JM;  
 XX DR WPI; 2002-657599/70.  
 XX PT New peptide inhibitors of p50/dynamitin useful for treating cancer by  
 PT inhibiting cellular proliferation, e.g. benign or malignant tumors,  
 PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and  
 PT immunologic disorders.

XX PS Claim 1; Page 29; 55pp; English.

XX The present invention describes an isolated peptide (I) comprising or  
 CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the  
 CC sequences given in ABP2966 and ABP52957 and can have C-terminal and N-  
 CC terminal extensions. (1) have cytostatic and antiinflammatory activities  
 CC and can be used as p50/dynamitin inhibitors and in gene therapy. The  
 CC peptides, nucleic acid molecules and methods from the present invention  
 CC are useful for treating cancer by inhibiting cellular proliferation, such  
 CC as benign or malignant tumours (renal, liver, kidney, bladder, breast,  
 CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and

CC neck tumours); leukaemias and lymphoid malignancies, other disorders such  
 CC as neuronal, glial, astrocytic, hypothalamic and other glandular,  
 CC macrophagal, epithelial, stromal and blastocoelic disorders; and  
 CC inflammatory, angiogenic and immunologic disorders. The present sequence  
 CC represents a peptide that can be N-terminally added to (P1)

SQ Sequence 22 AA;

Query Match 45.0%; Score 113; DB 5; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKETPQQKYQRLHLHEVQLTT 22  
 Db 1 GVKETPQQKYQRLHLHEVQLTT 22

RESULT 10

ABP52969  
 ID ABP52969 standard; peptide; 21 AA.

AC ABP52969;

XX DT 05-NOV-2002 (first entry)

DE Cellular proliferation inhibitor related peptide SEQ ID NO:4.

XX  
 KW Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;  
 KW p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma;  
 KW sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;  
 KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;  
 KW glandular disorder; macrophagal disorder; epithelial disorder;  
 KW stromal disorder; blastocoelic disorder; angiogenic disorder;

XX  
 KW immunologic disorder.

XX  
 Homo sapiens.

OS Mus musculus.

OS Synthetic.

XX WO200264779-A2.

XX PD 22-AUG-2002.

PP 21-JAN-2002; 2002WO-US001708.

XX PR 14-FEB-2001; 2001US-00782816.

XX PA (REGC ) UNIV CALIFORNIA.

XX PT Sharp DJ, Rogers GC, Scholey JM;

XX PI Sharp DJ, Rogers GC, Scholey JM;

XX PT WPI; 2002-657599/70.

XX PT New peptide inhibitors of p50/dynamitin useful for treating cancer by  
 PT inhibiting cellular proliferation, e.g. benign or malignant tumors,  
 PT leukemic and lymphoid malignancies, or inflammatory, angiogenic and  
 PT immunologic disorders.

XX PS Claim 1; Page 29; 55pp; English.

XX  
 CC The present invention describes an isolated peptide (I) comprising or  
 CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the  
 CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-  
 CC terminal extensions. (I) have cytostatic and antiinflammatory activities  
 CC and can be used as p50/dynamitin inhibitors and in gene therapy. The  
 CC peptides, nucleic acid molecules and methods from the present invention  
 CC are useful for treating cancer by inhibiting cellular proliferation, such  
 CC as benign or malignant tumours (renal, liver, kidney, bladder, breast,  
 CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva,  
 CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and  
 CC neck tumours), leukemias and lymphoid malignancies, other disorders such  
 CC as neuronal, glial, astrocytic, hypothalamic and other glandular,  
 CC macrophagal, epithelial, stromal and blastocoelic disorders; and  
 CC inflammatory, angiogenic and immunologic disorders. The present sequence  
 CC represents a peptide that can be N-terminally added to (P1)

CC inflammatory, angiogenic and immunologic disorders. The present sequence  
 CC represents a peptide that can be N-terminally added to (P1)

SQ Sequence 21 AA;

Query Match 42.6%; Score 107; DB 5; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKETPQQKYQRLHLHEVQLTT 22  
 Db 1 VKETPQQKYQRLHLHEVQLTT 21

RESULT 11

ABP52970  
 ID ABP52970 standard; peptide; 20 AA.

AC ABP52970;

XX DT 05-NOV-2002 (first entry)

DE Cellular proliferation inhibitor related peptide SEQ ID NO:5.

XX  
 KW Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;  
 KW p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma;  
 KW sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;  
 KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;  
 KW glandular disorder; macrophagal disorder; epithelial disorder;  
 KW stromal disorder; blastocoelic disorder; angiogenic disorder;  
 KW immunologic disorder.

XX  
 Homo sapiens.

OS Mus musculus.

OS Synthetic.

XX WO200264779-A2.

XX PD 22-AUG-2002.

PP 21-JAN-2002; 2002WO-US001708.

XX PR 14-FEB-2001; 2001US-00782816.

XX PA (REGC ) UNIV CALIFORNIA.

XX PT Sharp DJ, Rogers GC, Scholey JM;

XX PI Sharp DJ, Rogers GC, Scholey JM;

XX PT WPI; 2002-657599/70.

XX PT New peptide inhibitors of p50/dynamitin useful for treating cancer by  
 PT inhibiting cellular proliferation, e.g. benign or malignant tumors,  
 PT leukemic and lymphoid malignancies, or inflammatory, angiogenic and  
 PT immunologic disorders.

XX PS Claim 1; Page 29; 55pp; English.

CC The present invention describes an isolated peptide (I) comprising or  
 CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the  
 CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-  
 CC terminal extensions. (I) have cytostatic and antiinflammatory activities  
 CC and can be used as p50/dynamitin inhibitors and in gene therapy. The  
 CC peptides, nucleic acid molecules and methods from the present invention  
 CC are useful for treating cancer by inhibiting cellular proliferation, such  
 CC as benign or malignant tumours (renal, liver, kidney, bladder, breast,  
 CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva,  
 CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and  
 CC neck tumours), leukemias and lymphoid malignancies, other disorders such  
 CC as neuronal, glial, astrocytic, hypothalamic and other glandular,  
 CC macrophagal, epithelial, stromal and blastocoelic disorders; and  
 CC inflammatory, angiogenic and immunologic disorders. The present sequence  
 CC represents a peptide that can be N-terminally added to (P1)

SQ	Sequence 20 AA:	XN	Sequence 23 AA:
Query Match	41.0%;	Query Match	41.0%;
Best Local Similarity	100.0%;	Score	103;
Matches	Pred. No.	DB 5;	DB 5;
20;	4.5e-05;	Length	20;
Conservative	0;	Mismatches	0;
0;	Indels	0;	Gaps
QY	3	QY	23
	KETPQQKYQRLHENVQBLTT		EVEKIKTTVYESATEBEKLTPVUL
Db	22	Db	45
1	KETPQQKYQRLHENVQBLTT	1	EVEKIKTTVYESATEBEKLTPVUL
	20		23
RESULT 12		RESULT 13	
ABP52966		ABP52971	
ID ABP52966	standard; peptide; 23 AA.	ID ABP52971	standard; peptide; 19 AA.
XX		XX	
AC	ABP52966;	AC	ABP52971;
XX		XX	
DT	05-NOV-2002 (first entry)	DT	05-NOV-2002 (first entry)
DB	Cellular proliferation inhibitor related peptide SEQ ID NO:1.	DB	Cellular proliferation inhibitor related peptide SEQ ID NO:6.
XX		XX	
KW	Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;	KW	Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KW	p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma;	KW	p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma;
KW	sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;	KW	sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;
KW	glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;	KW	glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KW	glandular disorder; macrophagal disorder; epithelial disorder;	KW	glandular disorder; macrophagal disorder; epithelial disorder;
KW	stromal disorder; blastocoelic disorder; angiogenic disorder;	KW	stromal disorder; blastocoelic disorder; angiogenic disorder;
KW	immunologic disorder.	KW	immunologic disorder.
OS	Homo sapiens.	OS	Homo sapiens.
OS	Mus musculus.	OS	Mus musculus.
OS	Synthetic.	OS	Synthetic.
XX		XX	
FH		FH	
FT	Key Location/Qualifiers	FT	Key Location/Qualifiers
FT	Misc-difference 22	FT	Misc-difference 22
FT	/label= "Leu, Val	FT	/label= "Leu, Val
FT	/note= "Leu in humans and Val in Mus musculus"	FT	/note= "Leu in humans and Val in Mus musculus"
XX		XX	
PN	WO200264779-A2.	PN	WO200264779-A2.
XX		XX	
PD	22-AUG-2002.	PD	22-AUG-2002.
XX		XX	
PP	21-JAN-2002; 2002WO-US001708.	PP	21-JAN-2002; 2002WO-US001708.
XX		XX	
PR	14-FEB-2001; 2001US-00782816.	PR	14-FEB-2001; 2001US-00782816.
XX		XX	
PA	(REGC ) UNIV CALIFORNIA.	PA	(REGC ) UNIV CALIFORNIA.
XX		XX	
PI	Sharp DJ, Rogers GC, Scholey JM;	PI	Sharp DJ, Rogers GC, Scholey JM;
DR		DR	
XX		XX	
PT	New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.	PT	New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.
PT		PT	
PT	leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.	PT	leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.
PT		PT	
PT	New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.	PT	New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.
PT		PT	
PT	Inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.	PT	Inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.
PT		PT	
PT	Claim 1; Page 29; 55pp; English.	PT	Claim 1; Page 29; 55pp; English.
XX		XX	
CC	The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders; and, inflammatory, angiogenic and immunologic disorders. The present sequence represents a peptide that can be N-terminally added to (P1).	CC	The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders; and, inflammatory, angiogenic and immunologic disorders. The present sequence represents a peptide that can be N-terminally added to (P1).
CC	Sequence 19 AA;	CC	Sequence 19 AA;

Query Match 39.0%; Score 98; DB 5; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 0.00016;  
 Matches 19; Conservative 0; Mismatches 0; Indels 8

QY  
Dy  
Dy

5	TPOOKYQORLLHEVQELRTT	22
1	TPOOKYQORLLHEVQELRTT	18

Db 1 ETPOOKYQRLHENVQELTT 19

**RESULT 15**  
**ABP52973**

RESULT 14  
ABP52972  
ID ABP52972 standard; peptide; 18 AA.  
XX

XX  
AC  
XX  
DT 05-NOV-2002 (first entry)  
ABPF52973;

XX  
DT  
XX      05-NOV-2002 (first entry)

**XX** Cellular proliferation inhibitor related peptide SEQ ID NO:8.  
**KW** Cellular proliferation inhibition; cytostatic; antiinflammatory

**KW** p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma; sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder; KW glandular disorder; astrocytoma disorder; hypothalamic disorder; inflammatory; KW stromal disorder; macrophagal disorder; epithelial disorder; KW immunologic disorder.

**KW** stromal disorder; blastocoelic disorder; angiogenic disorder;  
**KW** immunologic disorder.

OS Homo sapiens.  
OS Mus musculus.  
OS Synthetic

*Mus musculus.*  
Synthetic.

PN  
XX  
PD  
23-DEC-2003

XX  
PD  
YY  
22-AUG-2002.

PF 21-JAN-2002; 2002WO-US001708  
XX  
PP 14 FEB 2001; 2001INC 00700016

XX  
PR  
VV  
14-FEB-2001; 2001US-00782816.

PA (REGC ) UNIV CALIFORNIA.  
XX

XX  
PI  
VV

DR WPI; 2002-657599/70.  
XX

**New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors,**

**PT** New peptide inhibitors of psu/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g., benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.

XX  
PS Claim 1; Page 29; 55pp; English.

PS  
XX  
CC  
CC  
Claim 1; Page 29; 55pp; English.  
The present invention describes a  
having at least 90% identity to

The present invention describes an isolated peptide (1) comprising or having at least 50% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP5266 and ABP5267 and can have C-terminal and N-terminal extensions. (1) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas, gliomatomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagai, epithelial, stromal and blastocoeleic disorders; and inflammatory, angiogenic and immunologic disorders. The present sequence represents a peptide that can be N-terminally added to (P1).

terminal extensions (T1) have cytostatic and anti-inflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastic, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocyt, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders; and inflammatory, angiogenic and immunologic disorders. The present sequence represents a peptide that can be N-terminally added to (P1)

SQ Sequence 18 A

Best Local Markets

Query Match Score 93%; DB 5; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 0.00058;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0

OY 6 PQQKYQRLLHEVQELTT 222

Mon Nov 7 09:42:37 2005

09782816-51.rag

Page 9

Db 1 PQQKYQRLAHENVQELTT 17

Search completed: November 3, 2005, 21:57:30  
Job time : 72.1872 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:32:33 ; Search time 41.0695 Seconds  
(without alignments)

282.516 Million cell updates/sec

Title: 09782816-1-22  
Perfect score: 1  
Sequence: EVERIKITIVKESATEEKLTIVPIAKOIAL 30  $\geq \chi_t = 0$

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04; \*

- 1: geneseqp1980s; \*
- 2: geneseqp1990s; \*
- 3: geneseqp2000s; \*
- 4: geneseqp2001s; \*
- 5: geneseqp2002s; \*
- 6: geneseqp2003ab; \*
- 7: geneseqp2003bs; \*
- 8: geneseqp2004s; \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query % Match Length	DB ID	Description
1	138	100.0	134 4 ARG77956	AAG75956 Human colo
2	138	100.0	314 8 ABM81421	Abm81421 Tumour-as
3	138	100.0	378 6 ABP9851	Abp9851 Human btr
4	138	100.0	401 7 ADU69563	Ad69563 Human hea
5	138	100.0	406 5 ABP53018	Abp53018 Human p50
6	138	100.0	465 3 ABP58368	Abp58368 Breast can
7	135	97.8	183 5 ABP53019	Abp53019 Mouse p50
8	133	96.4	52 5 ABP53016	Abp53016 Cellular
9	103	74.6	23 5 ABP52966	Abp52966 Cellular
10	56	40.6	334 6 ADB10226	Abd10226 Allotococ
11	51	37.0	932 6 ADU13229	Abu13229 Protein e
12	51	37.0	10917 6 ARB3632	Arae3632 Streptomy
13	50	36.2	210 3 ARG61007	Aarg61007 Arabidops
14	50	36.2	210 3 ARG1748	Aarg1748 Arabidops
15	50	36.2	6 6 ABU16767	Abu16767 Protein e
16	50	36.2	773 4 ARU3537	Aaru3537 Helicobac
17	50	36.2	773 6 ABU30798	Abu0798 Protein e
18	50	36.2	855 5 ARU9962	Aaru9962 Human His
19	50	36.2	855 7 ADC21699	Aadc21699 Human his
20	50	36.2	855 7 ADB9563	Adbs9563 Human his
21	50	36.2	912 8 ADH4346	Adh4346 Human cla
22	50	36.2	915 6 ABP56824	Abp56824 Human his
23	50	36.2	933 7 ABM85226	Abm85226 Mouse pro
24	50	36.2	938 8 ADT77693	Adt77693 Murine hi
25	50	36.2	1008 4 AAM78891	Aam78891 Human pro

**ALIGNMENTS**

RESULT 1  
AAG75956  
ID AAG75956 standard; protein; 134 AA.  
XX  
AC AAG75956;  
XX DT 03-SEP-2001 (first entry)  
XX DB Human colon cancer antigen protein SEQ ID NO:6720.  
XX HH Human; colon cancer; colon cancer antigen; diagnosis; detection;  
KW colorectal carcinoma; chromosome 12;  
XX OS Homo sapiens.  
XX PN WO200122220-A2.  
XX PD 05-APR-2001.  
XX PP 28-SEBP-2000; 2000W0-US026524.  
XX PR 29-SEP-1999; 99US-015137P.  
XX PR 03-NOV-1999; 99US-0163280P.  
XX PA (HUMAN) HUMAN GENOME SCI INC.  
XX PI Ruben SM, Barash SC, Birse CE, Rosen CA;  
XX DR WPI; 2001-235357/24.  
DR N-PSDB; AHM35361.  
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.  
XX PCT Claim 11; Page 8181; 9803pp; English.  
XX AAC2943 to AAH37195 and AAG73514 to AAG7788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytotoxic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P

CC	can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers.
CC	AAH37796 to AAH37204 and AAB77799 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922
CC	to 1052, 7921 and 7922
CC	Sequence 134 AA;
SQ	Query Match 100 %; Score 139; DB 4; Length 134; Best Local Similarity 100 %; Pred. No. 1.2e-11; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0 Qy 1 EVERKIKITVKSATERKUTPVLLAKQAL 30 Db 19 EVERKIKITVKSATERKUTPVLLAKQAL 48
RESULT 2	
ID ABM81421	
ID ABM81421 standard; protein; 314 AA.	
AC ABM81421;	
XX	
DT 18-NOV-2004 (first entry)	
XX	
DE Tumour-associated antigenic target (TAT) polypeptide PROB219L, SEQ:3675.	
XX	
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;	
KW tumor; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic.	
KW	
OS Homo sapiens.	
XX	
PN WO2004030615-A2.	
XX	
PD 15-APR-2004.	
XX	
PR 29-SBP-2003; 2003WO-US029547.	
XX	
PR 02-OCT-2002; 2002US-0414971P.	
XX	
PA (GETH ) GENENTECH INC.	
XX	
PI Wu TD, Zhang Z, Zhou Y;	
XX	
DR WPI; 2004-347921/32.	
DR N-PSDB; ACN39497.	
PS New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.	
XX	
Claim 12; SEQ ID NO 3675; 7273pp; English.	
CC The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with	

increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridization probes, in chromosome and gene mapping, in chromosomal identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention.

CC preventing diseases or conditions associated with the decreased  
 CC expression or over expression of SCAP, such as cell proliferative (e.g.  
 CC cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's  
 CC disease, stroke), heart (e.g. hypertension, heart failure, angina) and  
 CC skeletal muscle disorders (e.g. osteoporosis, osteoarthritis) or viral  
 CC infections. These are also useful in assessing the effects of exogenous  
 CC compounds on the expression of nucleic acid and amino acid sequences of  
 CC SCAP. The SCAP or its fragments are useful in screening compounds for  
 CC effectiveness as agonist or antagonist of the polypeptides, or in  
 CC altering the expression of the target polynucleotide and compounds that  
 CC specifically bind to or modulate the activity of the polypeptide. The  
 CC microarray is useful in monitoring or measuring protein-protein  
 CC interactions, drug-target interactions, and gene expression profiles  
 XX

SQ Sequence 378 AA;

Query Match 100.0%; Score 138; DB 6; Length 378;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-11;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEKIKTTVYESATEEKLTPVLLAKQAL 30  
 Db 93 EVEKIKTTVYESATEEKLTPVLLAKQAL 122

RESULT 4

ADD69563  
 ID ADD69563 Standard; protein; 401 AA.  
 XX  
 AC ADD69563;  
 XX  
 DT 06-MAY-2004 (first entry)

XX Human heat mitochondrial protein as a therapeutic target SeqID1369.  
 DE mitochondrial; human; screening assay; diabetes mellitus;  
 KW Huntington's disease; osteoarthritis;  
 KW Leber's hereditary optic neuropathy; LHN;  
 KW mitochondrial encephalopathy, lactic acidosis and stroke; MELAS;  
 KW myoclonic epilepsy; ragged red fibre syndrome; MERRF; cancer;  
 KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;  
 KW osteopathic; ophthalmological; cytopstatic.  
 XX OS Homo sapiens.  
 XX PN WO2003087768-A2.  
 XX PD 23-OCT-2003.  
 XX PP 04-APR-2003; 2003WO-US010870.  
 XX PR 12-APR-2002; 2002US-0372843P.  
 PR 17-JUN-2002; 2002US-0389987P.  
 PR 20-SEP-2002; 2002US-0412418P.  
 XX PR (RESC) UNIV CALIFORNIA.  
 XX PR Sharp DJ, Rogers GC, Schooley JM;  
 XX DR WPI; 2002-657599/70.

XX PT identifying a mitochondrial target for drug screening assays and for  
 PT comprising detecting a modified polypeptide in a sample and correlating  
 PT with the disease.  
 XX PS Claim 1; SEQ ID NO 1369; 180pp; English.

XX CC This invention relates to novel mitochondrial targets that can be used  
 CC for therapeutic intervention in treating a disease associated with an  
 altered mitochondrial function. Specifically, it refers to a method for  
 CC SQ Sequence 401 AA;

Query Match 100.0%; Score 138; DB 7; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-11;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEKIKTTVYESATEEKLTPVLLAKQAL 30  
 Db 116 EVEKIKTTVYESATEEKLTPVLLAKQAL 145

RESULT 5

ABP53018  
 ID ABP53018 Standard; protein; 406 AA.  
 XX  
 AC ABP53018;  
 XX  
 DT 05-NOV-2002 (first entry)

XX Human p50 amino acid sequence SEQ ID NO:53.  
 DE Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;  
 KW p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; Carcinoma;  
 KW sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;  
 KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;  
 KW glandular disorder; macrophagal disorder; epithelial disorder;  
 KW stromal disorder; blactocoelic disorder; angiogenic disorder;  
 KW immunologic disorder.  
 XX OS Homo sapiens.  
 XX PN WO200264779-A2.  
 XX PD 22-AUG-2002.  
 XX PP 21-JAN-2002; 2002WO-US001708.  
 XX PR 14-FEB-2001; 2001US-00782816.  
 XX PA (RESC) UNIV CALIFORNIA.  
 XX PR Sharp DJ, Rogers GC, Schooley JM;  
 XX DR WPI; 2002-657599/70.

XX PT New peptide inhibitors of p50/dynamitin useful for treating cancer by  
 PT inhibiting cellular proliferation, e.g. benign or malignant tumors,  
 PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and  
 PT immunologic disorders.

XX PS Disclosure; Fig 1; 55pp; English.

XX CC The present invention describes an isolated peptide (I) comprising or  
 having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the  
 CC sequences given in ABP5296 and ABP5397 and can have C-terminal and N-  
 terminal extensions. (I) have cytostatic and antiinflammatory activities  
 CC and can be used as p50/dynamitin inhibitors and in gene therapy. The  
 CC peptides, nucleic acid molecules and methods from the present invention  
 are useful for treating cancer by inhibiting cellular proliferation, such  
 CC as benign or malignant tumours (renal, liver, kidney, bladder, breast,

CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,  
 CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and  
 CC neck tumours; leukaemias and lymphoid malignancies, other disorders such  
 CC as neuronal, glial, astrocytal, hypothalamic and other glandular,  
 CC macrophagal, epithelial, stromal and blastocoelic disorders; and  
 CC inflammatory, angiogenic and immunologic disorders. The present sequence  
 CC represents human p50 which is given in the exemplification of the present  
 CC invention.

SQ Sequence 406 AA;

Query Match 100.0%; Score 138; DB 5; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-11; Mismatches 0;  
 Matches 30; Conservative 0; Indels 0; Gaps 0;

QY 1 EVEKIKITVKESESATEBKLTIPVLLAKQAL 30  
 Db 121 EVEKIKITVKESESATEBKLTIPVLLAKQAL 150

RESULT 6

AAB58968  
 ID AAB58968 standard; protein; 465 AA.  
 AC AAB58968;  
 XX

DT 27-MAR-2001 (first entry)

DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 676.  
 KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;  
 KW nootropic; neuroprotective; antiviral; antiallergic; hepatocropic;  
 KW anti-diabetic; anti-inflammatory; anti-ulcer; vulnerary; anticonvulsant;  
 KW antibiotic; antifungal; anti-parasitic; cardiot; immune disorder;  
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;  
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;  
 KW cardiovascular disorder; wound healing; neurological disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055173-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PP 08-MAR-2000; 2000WO-US005881.  
 XX  
 PR 12-MAR-1999; 99US-0124270P.

(HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 DR WPI; 2000-611515/58.  
 DR N-PSDB; AAP21871.

XX New human breast and ovarian cancer associated gene sequences and the  
 PT polypeptides encoded by these genes, useful in the prevention, treatment  
 PT and diagnosis of cancer, immune disorders, cardiovascular disorders and  
 PT neurological diseases.

XX  
 PS Claim 11; Page 1126-1128; 1299pp; English.

CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human  
 CC proteins AB58711 - AB55128. The DNA and protein sequences are  
 CC associated with breast and ovarian cancer. Included in the invention are  
 CC sequences AAF22032 - AAF22040 and AB559129 which are used in the  
 CC isolation and characterisation of the DNA and protein sequences of the  
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist  
 CC or antagonist sequences exhibit cytostatic; immunosuppressive; nontropic;  
 CC neuroprotective; antiviral; antiallergic; hepatocropic; anti-diabetic;  
 CC anti-inflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;  
 CC anti-fungal; antiparasitic and cardiot; activity. The polynucleotide and

CC protein sequences are used in the diagnosis of cancer, particularly  
 CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists  
 CC and antagonists may also be used in the diagnosis, prevention and treatment  
 CC of immune disorders e.g. Addison's disease, allergies, autoimmune  
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;  
 CC cardiovascular disorders such as myocardial ischaemias; wound healing;  
 CC neurological diseases such as cerebral anoxia and epilepsy; and  
 CC infectious diseases

SQ Sequence 465 AA;

Query Match 100.0%; Score 138; DB 3; Length 465;  
 Best Local Similarity 100.0%; Pred. No. 5e-11; Mismatches 0;  
 Matches 30; Conservative 0; Indels 0; Gaps 0; Gaps 0;

QY 1 EVEKIKITVKESESATEBKLTIPVLLAKQAL 30  
 Db 180 EVEKIKITVKESESATEBKLTIPVLLAKQAL 209

RESULT 7

ABP53019  
 ID ABP53019 standard; protein; 183 AA.  
 AC ABP53019;  
 XX

DT 05-NOV-2002 (first entry)

DR Mouse p50 amino acid sequence SEQ ID NO:54.  
 XX

KW Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;  
 KW p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma;  
 KW barcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;  
 KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;  
 KW glandular disorder; macrophagal disorder; epithelial disorder;  
 KW stromal disorder; blastocoelic disorder; angiogenic disorder;  
 KW immunologic disorder.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200264779-A2.  
 XX  
 PD 22-AUG-2002.  
 XX  
 PP 21-JAN-2002; 2002WO-US001708.  
 XX  
 PR 14-FEB-2001; 2001US-00782816.  
 XX  
 (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Sharp DJ, Rogers GC, Scholey JM;  
 XX  
 DR WPI; 2002-657599/70.  
 XX  
 PT New peptide inhibitors of p50/dynamitin useful for treating cancer by  
 PT inhibiting cellular proliferation, e.g. benign or malignant tumors'  
 PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and  
 PT immunologic disorders.

PS Disclosure; FIG 2; 55pp; English.

CC The present invention describes an isolated peptide (I) comprising or  
 CC having at least 90% identity to (P1) or (P2), where (P1) and (P2) are the  
 CC sequences given in ABP53019 and ABP5267 and can have C-terminal and N-  
 CC terminal extensions. (I) have cytostatic and antiinflammatory activities  
 CC and can be used as p50/dynamitin inhibitors and in gene therapy. The  
 CC peptides, nucleic acid molecules and methods from the present invention  
 CC are useful for treating cancer by inhibiting cellular proliferation, such  
 CC as benign or malignant tumours (renal, liver, bladder, breast,  
 CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, and various head and  
 CC neck tumours); leukaemias and lymphoid malignancies, other disorders such

CC as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders; and inflammatory, angiogenic and immunologic disorders. The present sequence represents mouse p50 which is given in the exemplification of the present invention.

XX Sequence 183 AA;

Query Match 97.8%; Score 135; DB 5; Length 183;  
Best Local Similarity 96.7%; Pred. No. 4.5e-11; 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEKIKTTVKEKESATEBEKLTPVLLAKQAL 30  
Db 116 EVEKIKTTVKEKESATEBEKLTPVLLAKQAL 145

RESULT 8

ABP53016  
ID ABP53016 standard; peptide; 52 AA.

XX ABP53016;  
XX DT 05-NOV-2002 (first entry)

DB Cellular proliferation peptide inhibitor SEQ ID NO:51.

XX KW Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; barcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder; ginal disorder; astrocytal disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder;

XX KW immunologic disorder.

OS Homo sapiens.

OS Mus musculus.

OS Synthetic.

OS

XX Key Location/Qualifiers

FH Misc-difference 44  
FT /label= Leu, Val  
PN /note= "Leu in humans and Val in Mus musculus"

WO200264779-A2.  
XX PD 22-AUG-2002.

XX PR 21-JAN-2002; 2002WO-US001708.

XX PR 14-FEB-2001; 2001US-00782816.

XX PA (RSGC ) UNIV CALIFORNIA.

XX PT Sharp DJ, Rogers GC, Schooley JM;  
DR Sharp DJ, Rogers GC, Schooley JM;

XX DR WPI; 2002-657599/70.

PT New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.

XX PS Claim 2; Page 31; 55pp; English.

CC The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cyrostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast,

CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcoma, glioblastomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders; and inflammatory, angiogenic and immunologic disorders. The present sequence represents a specifically claimed peptide inhibitor of cellular proliferation from the present invention.

XX Sequence 52 AA;

Query Match 96.4%; Score 133; DB 5; Length 52;  
Best Local Similarity 96.7%; Pred. No. 2e-11; 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEKIKTTVKEKESATEBEKLTPVLLAKQAL 30  
Db 23 EVEKIKTTVKEKESATEBEKLTPVLLAKQAL 52

RESULT 9

ABP52966  
ID ABP52966 standard; peptide; 23 AA.

XX ABP52966;  
XX DT 05-NOV-2002 (first entry)

DB Cellular proliferation inhibitor related peptide SEQ ID NO:1.

XX KW Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; barcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder; ginal disorder; astrocytal disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder; immunologic disorder.

XX OS Homo sapiens.

OS Mus musculus.

OS Synthetic.

XX Key Location/Qualifiers

FH Misc-difference 22  
FT /label= Leu, Val  
PN /note= "Leu in humans and Val in Mus musculus"

WO200264779-A2.  
XX PD 22-AUG-2002.

XX PR 21-JAN-2002; 2002WO-US001708.

XX PR 14-FEB-2001; 2001US-00782816.

XX PA (RSGC ) UNIV CALIFORNIA.

XX PT Sharp DJ, Rogers GC, Schooley JM;

XX DR WPI; 2002-657599/70.

PT New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.

XX PS Claim 1; Page 29; 55pp; English.

CC The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cyrostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast,

peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocyral, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoeleic disorders; and inflammatory, angiogenic and immunologic disorders.

SQ Sequence 23 AA;

Query Match 74.6%; Score 103; DB 5; Length 23;

Best Local Similarity 95.7%; Pred. No. 1.5e-07; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEKIKITTVKESATEBKLTIPULL 23

Db 1 EVEKIKITTVKESATEBKLTIPULL 23

RESULT 10

ADB10326

ID ADB10326 Standard; protein; 334 AA.

XX

AC ADB10326;

XX

DT 20-NOV-2003 (first entry)

XX

DE Alloiococcus otitis antigenic protein SBQ ID NO:4734.

XX

KW Alloiococcus otitis; antigenic protein; immunogenic; immunisation;

DB gene therapy; Gram-positive bacterium; infection.

OS Alloiococcus otitis.

XX

PN WO2003048304-A2.

XX

PD 12-JUN-2003.

XX

PP 25-NOV-2002; 2002WO-US036123.

XX

PR 29-NOV-2001; 2001US-0333777P.

XX

PR 18-NOV-2002; 2002US-0426742P.

XX

PA (AMER ) WYETH HOLDINGS CORP.

XX

PI Fletcher LD, McMichael JC, Russell DP, Zagursky RJ,

XX

DR WPI; 2003-505284/47.

DR

N-PSDB; ADB10329.

XX

PT New Alloiococcus otitis polyucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring of effects during drug clinical trials.

PT

PS Claim 33; SEQ ID NO 4734; 1019pp; English.

XX

CC The present invention describes an isolated polynucleotide (1) of

CC Alloiococcus otitis genomic DNA, which encodes an antigenic protein.

CC

CC An isolated polypeptide that is encoded by the polynucleotide (1), (2) an

CC expression vector comprising the novel isolated polynucleotide (1), its

CC complement, degenerate variant or fragment; (3) a genetically engineered

CC host cell, transfected, transformed or infected with the vector of (2);

CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic

CC composition comprising the polypeptide, its complement, biological

CC equivalent or fragment, or the polynucleotide that is comprised in the

CC expression vector; (6) a pharmaceutical composition comprising the

CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array

CC of the polypeptides of (1), their biological equivalent or fragment; (8)

CC immunising against Alloiococcus otitis by administering to a host the

CC immunogenic composition; (9) detecting and/or identifying Alloiococcus

CC SQ Sequence 23 AA;

Query Match 74.6%; Score 103; DB 5; Length 23;

Best Local Similarity 95.7%; Pred. No. 1.5e-07; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEKIKITTVKESATEBKLTIPULL 23

Db 1 EVEKIKITTVKESATEBKLTIPULL 23

RESULT 10

ADB10326

ID ADB10326 Standard; protein; 334 AA.

XX

AC ADB10326;

XX

DT 20-NOV-2003 (first entry)

XX

DE Alloiococcus otitis antigenic protein SBQ ID NO:4734.

XX

KW Alloiococcus otitis; antigenic protein; immunogenic; immunisation;

DB gene therapy; Gram-positive bacterium; infection.

OS Alloiococcus otitis.

XX

PN WO2003048304-A2.

XX

PD 12-JUN-2003.

XX

PP 25-NOV-2002; 2002WO-US036123.

XX

PR 29-NOV-2001; 2001US-0333777P.

XX

PR 18-NOV-2002; 2002US-0426742P.

XX

PA (AMER ) WYETH HOLDINGS CORP.

XX

PI Fletcher LD, McMichael JC, Russell DP, Zagursky RJ,

XX

DR WPI; 2003-505284/47.

DR

N-PSDB; ADB10329.

XX

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PT

PS Claim 33; SEQ ID NO 4734; 1019pp; English.

XX

CC The present invention describes an isolated polynucleotide (1) of

CC Alloiococcus otitis genomic DNA, which encodes an antigenic protein.

CC

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CC expression vector comprising the novel isolated polynucleotide (1), its

CC complement, degenerate variant or fragment; (3) a genetically engineered

CC host cell, transfected, transformed or infected with the vector of (2);

CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic

CC composition comprising the polypeptide, its complement, biological

CC equivalent or fragment, or the polynucleotide that is comprised in the

CC expression vector; (6) a pharmaceutical composition comprising the

CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array

CC of the polypeptides of (1), their biological equivalent or fragment; (8)

CC immunising against Alloiococcus otitis by administering to a host the

CC immunogenic composition; (9) detecting and/or identifying Alloiococcus

CC SQ Sequence 23 AA;

Query Match 74.6%; Score 103; DB 5; Length 23;

Best Local Similarity 95.7%; Pred. No. 1.5e-07; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEKIKITTVKESATEBKLTIPULL 23

Db 1 EVEKIKITTVKESATEBKLTIPULL 23

RESULT 10

ADB10326

ID ADB10326 Standard; protein; 334 AA.

XX

AC ADB10326;

XX

DT 20-NOV-2003 (first entry)

XX

DE Alloiococcus otitis antigenic protein SBQ ID NO:4734.

XX

KW Alloiococcus otitis; antigenic protein; immunogenic; immunisation;

DB gene therapy; Gram-positive bacterium; infection.

OS Alloiococcus otitis.

XX

PN WO2003048304-A2.

XX

PD 12-JUN-2003.

XX

PP 25-NOV-2002; 2002WO-US036123.

XX

PR 29-NOV-2001; 2001US-0333777P.

XX

PR 18-NOV-2002; 2002US-0426742P.

XX

PA (AMER ) WYETH HOLDINGS CORP.

XX

PI Fletcher LD, McMichael JC, Russell DP, Zagursky RJ,

XX

DR WPI; 2003-505284/47.

DR

N-PSDB; ADB10329.

XX

PT New Alloiococcus otitis polyucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring of effects during drug clinical trials.

PT

PS Claim 33; SEQ ID NO 4734; 1019pp; English.

XX

CC The present invention describes an isolated polynucleotide (1) of

CC Alloiococcus otitis genomic DNA, which encodes an antigenic protein.

CC

CC An isolated polypeptide that is encoded by the polynucleotide (1), (2) an

CC expression vector comprising the novel isolated polynucleotide (1), its

CC complement, degenerate variant or fragment; (3) a genetically engineered

CC host cell, transfected, transformed or infected with the vector of (2);

CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic

CC composition comprising the polypeptide, its complement, biological

CC equivalent or fragment, or the polynucleotide that is comprised in the

CC expression vector; (6) a pharmaceutical composition comprising the

CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array

CC of the polypeptides of (1), their biological equivalent or fragment; (8)

CC immunising against Alloiococcus otitis by administering to a host the

CC immunogenic composition; (9) detecting and/or identifying Alloiococcus

CC SQ Sequence 23 AA;

Query Match 74.6%; Score 103; DB 5; Length 23;

Best Local Similarity 95.7%; Pred. No. 1.5e-07; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEKIKITTVKESATEBKLTIPULL 23

Db 1 EVEKIKITTVKESATEBKLTIPULL 23

RESULT 10

ADB10326

ID ADB10326 Standard; protein; 334 AA.

XX

AC ADB10326;

XX

DT 20-NOV-2003 (first entry)

XX

DE Alloiococcus otitis antigenic protein SBQ ID NO:4734.

XX

KW Alloiococcus otitis; antigenic protein; immunogenic; immunisation;

DB gene therapy; Gram-positive bacterium; infection.

OS Alloiococcus otitis.

XX

PN WO2003048304-A2.

XX

PD 12-JUN-2003.

XX

PP 25-NOV-2002; 2002WO-US036123.

XX

PR 29-NOV-2001; 2001US-0333777P.

XX

PR 18-NOV-2002; 2002US-0426742P.

XX

PA (AMER ) WYETH HOLDINGS CORP.

XX

PI Fletcher LD, McMichael JC, Russell DP, Zagursky RJ,

XX

DR WPI; 2003-505284/47.

DR

N-PSDB; ADB10329.

XX

PT New Alloiococcus otitis polyucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring of effects during drug clinical trials.

PT

PS Claim 33; SEQ ID NO 4734; 1019pp; English.

XX

CC The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC

CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) CC identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [http://wipo.int/pub/published\\_pc\\_t\\_sequences](http://wipo.int/pub/published_pc_t_sequences)

## Sequence 932 AA;

Query Match

Best Local Similarity 37.0%; Pred. No. 2.9e+02; Length 932; Matches 11; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 2 VEKIKITVVKESATEBKLTPLVTLAKQLAAL 30  
 Db 397 IDKIDKATKEYIKNKLTPKLAQEGAM 425

## RESULT 12

AAB36132 standard; protein; 10917 AA.

AC AAB36132;

DT 26-JUN-2003 (first entry)

DE Streptomyces nodosus amphiC gene encoded protein.

KW Polyene; antibiotic; amphotericin; amph; polyketide synthase; enzyme.

XX Streptomyces nodosus.

PN WO200291082\_A2.

PD 05-DEC-2002.

XX PF 27-MAY-2002; 2002WO-IE000071.

XX PR 31-MAY-2001; 2001IE-00000527.

XX PA (YUDU-) UNIV COLLEGE DUBLIN.

PI Caffrey JP;

XX DR WPI; 2003-201271/19.

DR N-PSDB; AADS54645.

XX Novel cytochrome P450 enzyme and nucleotides encoding the enzyme, useful for preparing amphotericin derivative or analog antibiotic agent with altered properties, in biosynthesis of polyketide other than amphotericin.

PS Claim 6; Page 227-276; 276PP; English.

XX The invention relates to the gene cluster encoding the polypeptides responsible for the biosynthesis of the polyene antibiotic amphotericin (amph) of Streptomyces nodosus. Polynucleotides of the invention are useful for preparing amphotericin derivatives or analogue antibiotic

CC agents with altered properties and in the biosynthesis of polyketides other than amphotericin. amphiDII, amphiDI or amphiI mutants are useful for producing amphotericin derivatives glycosylated with alternative sugars; amphiII or amphiDI gene sequences are useful in engineered biosynthesis of perosaminyl-amphoteronolide B; amphiII or amphiI and amphi gene sequences are useful in the engineered biosynthesis of perosaminyl-16-decarboxyl-1'-methyl amphoteronolide B; amphiDII and amphiI gene sequences are useful for preparing polypeptides capable of addition of mycosamine to a polyketide other than amphoteronolide A or B or for preparing polypeptides for in vitro synthesis of GDP-mycosamine. The present sequence is a polyketide synthase multi-enzyme housing extension modules 3, 4, 5, 6, 7 and 8 encoded by S. nodosus amphiC gene sequence 10917 AA;

Query Match Best Local Similarity 37.0%; Pred. No. 5.1e+03; Length 10917; Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 5 IKTTWKESETEKKITPVLAKQLAAL 30  
 Db 1633 IRTTVRRAAAQSVTADGLAQLAGL 1658

## RESULT 13

AAG6107 standard; protein; 210 AA.

AC AAG6107;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SBQ ID NO: 79081.

KW Protein identification; signal transduction pathway; metabolic pathway; hybridization assay; genetic mapping; gene expression control; promoter; termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033495-A2.

PD 06-SEP-2000.

XX PP 25-FEB-2000; 2000BRP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 23-APR-1999; 99US-0130891P.

PR 30-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132043P.

PR 04-MAY-1999; 99US-0132407P.

PR 05-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

PR 07-MAY-1999; 99US-0132863P.

PR 11-MAY-1999; 99US-0134256P.

PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134221P.

PR 14-MAY-1999; 99US-0134370P.

PR	18-MAY-1999;	990US-0134768P.	PR	27-JUL-1999;	990US-0145919P.
PR	19-MAY-1999;	990US-0134941P.	PR	28-JUL-1999;	990US-0145951P.
PR	20-MAY-1999;	990US-0135124P.	PR	02-AUG-1999;	990US-0146386P.
PR	21-MAY-1999;	990US-0135353P.	PR	02-AUG-1999;	990US-0146388P.
PR	24-MAY-1999;	990US-0135629P.	PR	02-AUG-1999;	990US-0146389P.
PR	25-MAY-1999;	990US-0136021P.	PR	03-AUG-1999;	990US-0147038P.
PR	27-MAY-1999;	990US-0136392P.	PR	04-AUG-1999;	990US-0147204P.
PR	28-MAY-1999;	990US-0136782P.	PR	04-AUG-1999;	990US-0147302P.
PR	01-JUN-1999;	990US-0137222P.	PR	05-AUG-1999;	990US-0147192P.
PR	03-JUN-1999;	990US-0137528P.	PR	05-AUG-1999;	990US-0147260P.
PR	04-JUN-1999;	990US-0137502P.	PR	06-AUG-1999;	990US-0147303P.
PR	07-JUN-1999;	990US-0137724P.	PR	06-AUG-1999;	990US-0147416P.
PR	08-JUN-1999;	990US-0138094P.	PR	09-AUG-1999;	990US-0147433P.
PR	10-JUN-1999;	990US-0138540P.	PR	09-AUG-1999;	990US-0147935P.
PR	10-JUN-1999;	990US-0138847P.	PR	10-AUG-1999;	990US-0148171P.
PR	14-JUN-1999;	990US-0139119P.	PR	11-AUG-1999;	990US-0148199P.
PR	16-JUN-1999;	990US-0139528P.	PR	12-AUG-1999;	990US-0148341P.
PR	16-JUN-1999;	990US-0139452P.	PR	13-AUG-1999;	990US-0148565P.
PR	17-JUN-1999;	990US-0139453P.	PR	13-AUG-1999;	990US-0148684P.
PR	18-JUN-1999;	990US-0139492P.	PR	16-AUG-1999;	990US-0149368P.
PR	18-JUN-1999;	990US-0139460P.	PR	17-AUG-1999;	990US-0149461P.
PR	18-JUN-1999;	990US-0139455P.	PR	18-AUG-1999;	990US-0149426P.
PR	18-JUN-1999;	990US-0139462P.	PR	20-AUG-1999;	990US-0149722P.
PR	18-JUN-1999;	990US-0139463P.	PR	20-AUG-1999;	990US-0149723P.
PR	18-JUN-1999;	990US-0139458P.	PR	20-AUG-1999;	990US-0149844P.
PR	18-JUN-1999;	990US-0139459P.	PR	23-AUG-1999;	990US-0149368P.
PR	18-JUN-1999;	990US-0139461P.	PR	23-AUG-1999;	990US-0149930P.
PR	18-JUN-1999;	990US-0139462P.	PR	25-AUG-1999;	990US-0150565P.
PR	18-JUN-1999;	990US-0139463P.	PR	26-AUG-1999;	990US-0149722P.
PR	18-JUN-1999;	990US-0139750P.	PR	27-AUG-1999;	990US-0150655P.
PR	18-JUN-1999;	990US-0139763P.	PR	27-AUG-1999;	990US-0151066P.
PR	21-JUN-1999;	990US-0139817P.	PR	27-AUG-1999;	990US-0151080P.
PR	22-JUN-1999;	990US-0139899P.	PR	30-AUG-1999;	990US-0151303P.
PR	23-JUN-1999;	990US-0140353P.	PR	31-AUG-1999;	990US-0151438P.
PR	01-JUL-1999;	990US-0140354P.	PR	01-SEP-1999;	990US-0151930P.
PR	13-JUN-1999;	990US-0140695P.	PR	07-SEP-1999;	990US-0152363P.
PR	18-JUN-1999;	990US-0140695P.	PR	27-AUG-1999;	990US-0151999P.
PR	28-JUN-1999;	990US-0140823P.	PR	27-AUG-1999;	990US-0153758P.
PR	29-JUN-1999;	990US-0140991P.	PR	15-SEP-1999;	990US-0154018P.
PR	30-JUN-1999;	990US-0141287P.	PR	16-SEP-1999;	990US-0154039P.
PR	01-JUL-1999;	990US-0141842P.	PR	20-SEP-1999;	990US-0154779P.
PR	12-JUL-1999;	990US-0142154P.	PR	22-SEP-1999;	990US-0155139P.
PR	02-JUL-1999;	990US-0142055P.	PR	23-SEP-1999;	990US-0155307P.
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PR	09-JUL-1999;	990US-0142920P.	PR	29-SEP-1999;	990US-0156596P.
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PR	16-JUL-1999;	990US-0144086P.	PR	08-OCT-1999;	990US-0158232P.
PR	19-JUL-1999;	990US-0144335P.	PR	12-OCT-1999;	990US-0158369P.
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PR	20-JUL-1999;	990US-0144352P.	PR	14-OCT-1999;	990US-0159294P.
PR	20-JUL-1999;	990US-0144632P.	PR	13-OCT-1999;	990US-0159295P.
PR	20-JUL-1999;	990US-0144884P.	PR	14-OCT-1999;	990US-0159331P.
PR	21-JUL-1999;	990US-0145192P.	PR	14-OCT-1999;	990US-0159637P.
PR	21-JUL-1999;	990US-0145086P.	PR	14-OCT-1999;	990US-0159638P.
PR	21-JUL-1999;	990US-0145218P.	PR	21-OCT-1999;	990US-0160767P.
PR	23-JUL-1999;	990US-0145224P.	PR	21-OCT-1999;	990US-0160768P.
PR	22-JUL-1999;	990US-0145087P.	PR	21-OCT-1999;	990US-0160769P.
PR	22-JUL-1999;	990US-0145276.	PR	21-OCT-1999;	990US-0161405P.
PR	27-JUL-1999;	990US-0145513P.	PR	25-OCT-1999;	990US-0161406P.
PR	27-JUL-1999;	990US-0145518P.	PR	25-OCT-1999;	990US-0161406P.

PR	26-OCT-1999;	99US-0161359P.	PR	28-MAY-1999;	99US-0136782P.	
PR	26-OCT-1999;	99US-0161360P.	PR	01-JUN-1999;	99US-013722P.	
PR	26-OCT-1999;	99US-0161361P.	PR	03-JUN-1999;	99US-0137528P.	
PR	28-OCT-1999;	99US-0161920P.	PR	04-JUN-1999;	99US-0137502P.	
PR	28-OCT-1999;	99US-0161922P.	PR	07-JUN-1999;	99US-0137724P.	
PR	28-OCT-1999;	99US-0161993P.	PR	08-JUN-1999;	99US-0138094P.	
PR	29-OCT-1999;	99US-0162142P.	PR	10-JUN-1999;	99US-0138540P.	
<b>Query Match</b>			<b>Score</b>	<b>50;</b>	<b>DB 3;</b>	
<b>Best Local Matches</b>	<b>Similarity</b>	<b>36.2%;</b>	<b>Length</b>	<b>210;</b>		
<b>9;</b>	<b>Conservative</b>	<b>50.0%;</b>	<b>Fre. No.</b>	<b>71;</b>		
<b>9;</b>	<b>Mismatches</b>	<b>5;</b>	<b>Indels</b>	<b>4;</b>		
<b>OY</b>	<b>1</b>	<b>EVEKIKTTVKESEATEKL</b>	<b>18</b>	<b>0;</b>	<b>Gaps</b>	<b>0;</b>
<b>Db</b>	<b>174</b>	<b>EPERVKIMIEBFLTEK1</b>	<b>191</b>			
<b>RESULT 14</b>						
AAG17748	XX	Arabidopsis thaliana protein fragment SEQ ID NO: 18886.	XX	XX	XX	XX
ID	AAG17748	standard; protein; 210 AA.	XX	XX	XX	XX
AC	AAG17748;					
XX						
DT	17-OCT-2000	(first entry)				
XX						
XX						
DB	Arabidopsis thaliana	protein fragment SEQ ID NO: 18886.	KW	protein identification; signal transduction pathway; metabolic pathway;	KW	hybridization assay; genetic mapping; gene expression control; promoter;
XX			termination sequence.			
KW						
OS	Arabidopsis thaliana.					
XX						
PN	EP1033405-A2.					
XX						
PD	06-SEP-2000.					
XX						
PF	25-FEB-2000;	2000EP-00301439.				
XX						
PR	25-FEB-1999;	99US-0121825P.				
PR	05-MAR-1999;	99US-0123180P.				
PR	09-MAR-1999;	99US-0123548P.				
PR	23-MAR-1999;	99US-0125788P.				
PR	25-MAR-1999;	99US-0126264P.				
PR	29-MAR-1999;	99US-0126785P.				
PR	01-APR-1999;	99US-0127462P.				
PR	06-APR-1999;	99US-0128234P.				
PR	08-APR-1999;	99US-0128714P.				
PR	16-APR-1999;	99US-0129845P.				
PR	19-APR-1999;	99US-0130077P.				
PR	21-APR-1999;	99US-013049P.				
PR	23-APR-1999;	99US-0130510P.				
PR	23-APR-1999;	99US-0130891P.				
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PR	04-MAY-1999;	99US-0132407P.				
PR	05-MAY-1999;	99US-0132485P.				
PR	06-MAY-1999;	99US-0132486P.				
PR	06-MAY-1999;	99US-0132487P.				
PR	07-MAY-1999;	99US-0132863P.				
PR	11-MAY-1999;	99US-0134256P.				
PR	14-MAY-1999;	99US-0134219P.				
PR	14-MAY-1999;	99US-0134221P.				
PR	14-MAY-1999;	99US-0134370P.				
PR	18-MAY-1999;	99US-014768P.				
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PR	20-MAY-1999;	99US-0135124P.				
PR	21-MAY-1999;	99US-0135353P.				
PR	24-MAY-1999;	99US-0135629P.				
PR	25-MAY-1999;	99US-0136021P.				
PR	27-MAY-1999;	99US-0136392P.				

PR 04-AUG-1999; 99US-0147302P.  
 PR 05-AUG-1999; 99US-0147192P.  
 PR 05-AUG-1999; 99US-0147260P.  
 PR 06-AUG-1999; 99US-0147305P.  
 PR 09-AUG-1999; 99US-0147416P.  
 PR 10-AUG-1999; 99US-0147493P.  
 PR 11-AUG-1999; 99US-0148319P.  
 PR 12-AUG-1999; 99US-0148341P.  
 PR 13-AUG-1999; 99US-0148565P.  
 PR 13-AUG-1999; 99US-0148684P.  
 PR 15-AUG-1999; 99US-0149368P.  
 PR 17-AUG-1999; 99US-0149175P.  
 PR 20-AUG-1999; 99US-0149426P.  
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 PR 23-AUG-1999; 99US-0149929P.  
 PR 23-AUG-1999; 99US-0149902P.  
 PR 25-AUG-1999; 99US-0149930P.  
 PR 26-AUG-1999; 99US-0150566P.  
 PR 27-AUG-1999; 99US-0150884P.  
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 PR 27-AUG-1999; 99US-0151066P.  
 PR 30-AUG-1999; 99US-0151303P.  
 PR 31-AUG-1999; 99US-0151438P.  
 PR 01-SEP-1999; 99US-0151930P.  
 PR 07-SEP-1999; 99US-0152363P.  
 PR 10-SEP-1999; 99US-0152070P.  
 PR 13-SEP-1999; 99US-0153758P.  
 PR 15-SEP-1999; 99US-0154018P.  
 PR 16-SEP-1999; 99US-0154039P.  
 PR 20-SEP-1999; 99US-0154779P.  
 PR 22-SEP-1999; 99US-0155139P.  
 PR 23-SEP-1999; 99US-0155486P.  
 PR 24-SEP-1999; 99US-0156569P.  
 PR 28-SEP-1999; 99US-0156458P.  
 PR 29-SEP-1999; 99US-0156596P.  
 PR 04-OCT-1999; 99US-0157117P.  
 PR 05-OCT-1999; 99US-0157753P.  
 PR 06-OCT-1999; 99US-0157865P.  
 PR 07-OCT-1999; 99US-0158029P.  
 PR 08-OCT-1999; 99US-0158232P.  
 PR 12-OCT-1999; 99US-0158330P.  
 PR 13-OCT-1999; 99US-0158293P.  
 PR 13-OCT-1999; 99US-0158294P.  
 PR 13-OCT-1999; 99US-0158295P.  
 PR 14-OCT-1999; 99US-0158331P.  
 PR 14-OCT-1999; 99US-0158637P.  
 PR 14-OCT-1999; 99US-0158638P.  
 PR 18-OCT-1999; 99US-0158584P.  
 PR 21-OCT-1999; 99US-0160741P.  
 PR 21-OCT-1999; 99US-0160767P.  
 PR 21-OCT-1999; 99US-0160768P.  
 PR 21-OCT-1999; 99US-0160770P.  
 PR 21-OCT-1999; 99US-0160814P.  
 PR 21-OCT-1999; 99US-0160815P.  
 PR 22-OCT-1999; 99US-0160980P.  
 PR 22-OCT-1999; 99US-0160981P.  
 PR 22-OCT-1999; 99US-0160989P.  
 PR 25-OCT-1999; 99US-0161404P.  
 PR 25-OCT-1999; 99US-0161405P.  
 PR 25-OCT-1999; 99US-0161406P.  
 PR 26-OCT-1999; 99US-0161359P.  
 PR 26-OCT-1999; 99US-0161360P.  
 PR 26-OCT-1999; 99US-0161361P.  
 PR 28-OCT-1999; 99US-0161920P.  
 PR 28-OCT-1999; 99US-0161922P.  
 PR 28-OCT-1999; 99US-0161932P.  
 PR 28-OCT-1999; 99US-0161933P.  
 PR 29-OCT-1999; 99US-0162142P.

Query Match 36.2%; Score 50; DB 3; Length 210;  
 Best Local Similarity 50.0%; Pred. No. 71; Mismatches 4; Indels 0; Gaps 0;  
 Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy	1	EVEKIKTTVKESEWEEKL	18
Db	174	EPERVKTMIEBEFLTEEKI	191

**RESULT 15**  
**ABU16767**  
**ID ABU16767 standard; protein; 640 AA.**  
**XX**  
**AC ABU16767;**  
**XX**  
**DT 19-JUN-2003 (first entry)**  
**XX**  
**DE protein encoded by Prokaryotic essential gene #2294.**  
**XX**  
**KW Antisense; prokaryotic essential gene; cell proliferation; drug design.**  
**XX**  
**OS Acinetobacter baumannii.**  
**XX**  
**PN WO200277183-A2.**  
**XX**  
**PD 03-OCT-2002.**  
**XX**  
**PP 21-MAR-2002; 2002WO-US009107.**  
**XX**  
**PR 21-MAR-2001; 2001US-00815242.**  
**PR 06-SEP-2001; 2001US-00348993.**  
**PR 25-OCT-2001; 2001US-0342923P.**  
**PR 08-FEB-2002; 2001US-00072851.**  
**PR 06-MAR-2002; 2001US-0362699P.**  
**XX**  
**PA (ELIT-) ELITRA PHARM INC.**  
**XX**  
**PT Wang L, Zamudio C, Malone C, Haselbeck R, Ohlseni KL, Zyskind JW,**  
**PT Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;**  
**XX**  
**WPI; 2003-029926/02.**  
**DR N-P5DB; ACA20637.**  
**XX**  
**PS Claim 25; SEQ ID NO 44791; 176pp; English.**

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pot\_sequences  
XX  
SQ Sequence 640 AA:

Query Match 35.2%; Score 50; DB 6; Length 640;  
Best Local Similarity 39.3%; Pred. No. 2.6e+02;  
Matches 11; Conservative 7; Mismatches 10; Indels 0; Gaps 0;  
QY 3 EKIKITVKGESATEEKITPVNLAKQIAAL 30  
Db 131 DRYQKLVKERASDEBITQHLMMPMIRAL 158

Search completed: November 3, 2005, 21:57:27  
Job time : 44.0695 secs

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GenCore version 5.1.6  
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**OM protein - protein search, using SW model**

Run on: November 3, 2005, 21:43:09 ; Search time 10.9091 Seconds  
 (without alignment)  
 264.596 Million cell updates/sec

Title: 09782816-1-22  
 Perfect score: 138  
 Sequence: 1 EVEKIKTVKESATEKUTPVVLAQQLAL 30  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext: 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_79,\*  
 1: pir1,\*  
 2: pir2,\*  
 3: pir3,\*  
 4: pir4,\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	53	38.4	1394	hypothetical protein F28B3.1 - <i>Caenorhabditis elegans</i>
2	51	37.0	773	DNA gyrase chain B
3	51	37.0	932	penicillin-binding protein
4	50.5	36.6	191	lipopeptide-protein II
5	50.5	36.6	191	hypothetical protein
6	50	36.2	210	DNA gyrase, sub B
7	50	36.2	773	hypothetical protein
8	50	36.2	2	T117245
9	49	35.5	1151	probable peptidoglycan hydrolase
10	49	35.5	298	carboxyphosphonate
11	49	35.5	340	hypothetical protein
12	48.5	35.1	455	probable agx-1 homolog
13	48	34.8	311	primosome component
14	48	34.8	211	hypothetical prote
15	48	34.8	379	hypothetical prote
16	48	34.8	1112	cell division cont
17	48	34.8	1287	hypothetical prote
18	47.5	34.4	2	posterior-group pr
19	47	34.1	225	hypothetical prote
20	47	34.1	2	ribosomal protein
21	47	34.1	103	hypothetical prote
22	47	34.1	138	hypothetical prote
23	47	34.1	2	probable translati
24	47	34.1	2515	acetyl-CoA carboxy
25	47	34.1	2	glutamine synthetase
26	47	34.1	697	nuclear distribution
27	46.5	33.7	761	translation elonga
28	46.5	33.7	1	hydroxymethylgluta
29	46.5	33.7	453	hypothetical prote
	2	33.7	2	notch4 - mouse
	2	33.7	1964	
	2	33.7	T09059	

#### ALIGNMENTS

hypothetical prote  
 protein F59A7.4 [i  
 phosphoprotein pho  
 signal recognition  
 hypothetical prote  
 protein YKR029C ho  
 CBL-like protein  
 DNA topoisomerase  
 hypothetical prote  
 secretory compone  
 polymeric immunogl  
 Ca2+-transporting  
 probable peptidogly  
 protein T6D2.14 [i  
 histone H1.4 - Cae  
 protein C18G1.5 [i

RESULT 1  
 T34061  
 hypothetical protein F28B3.1 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T34061  
 R;Geisel, C.; Kramer, J.; Smith, A.  
 submitted to the EMBL Data Library, May 1997

A;Description: The sequence of *C. elegans* cosmid F28B3.  
 A;Reference number: Z21469  
 A;Accession: T34061  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-1394 <GET>

A;Cross-References: UNIPROT:Q01787; EMBL:AF003136; PIDN:AAH93631.1; GSPDB:GN00019; CESP:

A;Experimental source: strain Bristol N2; clone F28B3

C;Genetics

A;Gene: CESP:F28B3.1

A;Map position: 1

A;Introns: 46/3; 105/2; 280/3; 337/1; 358/1; 530/3; 685/3; 789/3; 1311/2

Query Match Score: 38.4%; DB 2; Length 1394;  
 Best Local Similarity 40.9%; Pred. No. 67; Mismatches 6; Indels 0; Gaps 0;

Matches 9; Conservative 7; Mismatches 6; Indels 0; Gaps 0;  
 QY            3 EKIKTVKESATEKUTPVVLA 24  
 |::|:|||:|||:|||:|||:  
 Db            1370 EKLRSITRSFLKEKUNPIVVA 1391

RESULT 2  
 T34061

DNA gyrase chain B - *Helicobacter pylori* (strain J99)  
 C;Species: *Helicobacter pylori*

A;Variety: strain J99

C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004

C;Accession: B71931

R;Aim, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature, 397, 176-180, 1999  
 A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen  
 A;Reference number: A71800; MUID:99120557; PMID:9923682  
 A;Accession: B71931  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residue: 1-773 <ARN>

A;Cross-references: UNIPROT:Q9ZLX3; GB:AE001479; PIDN:AA0603  
 A;Experimental source: strain J99

C;Genetics

A;Gene: GYRB

C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B

Query Match 37.0%; Score 51; DB 2; Length 773;  
best local similarity 43.5%; Bred. No. 66;  
Matches 10; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 5 IKTIVKTVKESATEEKLTIPVLLAKQL 27  
Db 222 LKQFVKDSAKELLTPISIIFKSM 244

RESULT 3

penicillin-binding protein (pbp-3) homolog - lyme disease spirochete.

C;Species: *Borrelia burgdorferi* (Lyme disease spirochete)  
C;Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 09-Jul-2004  
C;Accession: C70191

R;Fraser, C.M.; Caijens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, D.; Peterson, J.; Kerlavage, A.R.; Quachienbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997;  
A;Authors: Smith, H.O.; Venter, J.C.  
A;Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.  
A;Reference number: A70100; MUID:98065943; PMID:9403685

A;Accession: C70191

A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-932 <KLE>  
A;Cross-references: UNIPROT:051674; GB:AE001173; GB:AB000783; NID:92688665; PIDN: AAC6708  
A;Experimental source: strain B31

Query Match 37.0%; Score 51; DB 2; Length 932;  
Best Local Similarity 37.9%; Pred. No. 81;  
Matches 11; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 2 VEKIKTVKESATEEKLTIPVLLAKQL 30  
Db 397 IDKIKRATKEVTEIKNKLTPKLAQPGAM 425

RESULT 4

lipopeptide-protein ligase B (lipopeptide biosynthesis protein B) [imported] - *Salmonella enterica*

C;Species: *Salmonella enterica* subsp. *enterica* serovar *Typhi*  
C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C;Accession: AF0580

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, Th., Parkhill, J.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Molle, S.; O'Gaora, P. Nature 413, 848-852, 2001.  
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar *Infantis*.  
A;Reference number: AB0502; MUID:21534947; PMID:11677608  
A;Accession: AF0580  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-191 <PAR>  
A;Cross-references: GB:AL513382; PIDN: CAD05112.1; PID:gi16501886; GSPDB:GN00176  
C;Genetics:  
C;Superfamily: Escherichia coli lipopeptide-protein ligase lbp

Query Match 36.6%; Score 50.5%; DB 2; Length 191;  
Best Local Similarity 50.0%; Pred. No. 17;  
Matches 15; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 1 EVEKIKTVKESATEEKLTIPVLLAKQL 30  
Db 153 EMAKI-TQWKEADATTQDNIAPPRLANILALL 181

RESULT 5

hypothetical protein At2g11890 [imported] - *Arabidopsis thaliana*

E84499

Query Match 36.2%; Score 50; DB 2; Length 773;  
best local similarity 43.5%; Bred. No. 90;  
Matches 10; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 5 IKTIVKTVKESATEEKLTIPVLLAKQL 27  
Db 222 LKQFVKDSAKELLTPISIIFKSM 244

RESULT 6

DNA gyrase, sub B - *Helicobacter pylori* (strain 2665)

C;Species: *Helicobacter pylori*  
C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
C;Accession: B64582

R;Tomb, J.F.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L. Nature 388, 539-547, 1997  
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.  
A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-773 <TOM>  
A;Cross-references: UNIPROT:P55992; GB:AE000564; GB:AE000511; NID:92313602; PIDN:AD0756  
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B

Query Match 36.2%; Score 50; DB 2; Length 773;  
Best Local Similarity 43.5%; Pred. No. 90;  
Matches 10; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 5 IKTIVKTVKESATEEKLTIPVLLAKQL 27  
Db 222 LKQFVKDSAKELLTPISIIFKSM 244

RESULT 7

hypothetical protein T17245

C;Species: *Homo sapiens* (man)  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T17245

R;Koehler, K.; Beyer, A.; Mewes, H.W.; Gaasenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, September 1999  
A;Reference number: Z18722  
A;Accession: T17245  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-878 <KOE>  
A;Cross-references: EMBL:AL117455  
A;Experimental source: adult uterus; clone DKF2p586n0917  
C;Genetics:

A; Note: DKFZp586J0917.1

A;Contents: annotations

Query Match Score 50; DB 2; Length 878;

C;Genetics:  
A;Gene: XFL1234

QY 2 VEKIKTTVKEEATTEKLTIPVLAQKQL 30  
 C-terminal: carboxyphosphoinosipolyribose phosphotransferase  
 Query Match Similarity 35.5%; Score 49; DB 2; Length 298;  
 Best Local Similarity 41.4%; Pred. No. 44; Mismatches 11; Indels 0; Gaps 0;  
 Matches 12; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

AGI/17  
Astronomical Society of the Pacific  
1993 Meeting Program

Prospecie Peptidoglycan bound protein (M6A1G motif) L11m263 [Imported] - *Listeria innocua* C;Species: *Listeria* innocua C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004 Arrangement: ACII7

RESULT 10  
T4684 human fragment D46841 - human (fragment).

R; Giacobini, P.; Horaux, J.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloemberger, R.; Glaser, P.; Franque, L.; Duchaud, E.; Durand, L.; Dussarbez, O.; Entian, K.D.; Faihi, H.; Dominguez-Bernal, G.; Dominguez-Bernal, G.; T.M.; Karst, M.

C;SPECIES: Homo Sapiens (man)  
C;DATE: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004

Science 224, 849-852, 2001  
A;Authors: Kreft, J.J.; Kuhn, M.; Kunst, F.; Kurppkat, G.; Madiueno, E.; Maitournam, A.; Ma-  
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wenland,  
A;Title: Comparative Genomics of *Listeria* Species  
A;Reference number: AB1077; MUID:21537279; PMID:11679669  
A;Accession: AC1717  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1151<GLA>  
A;Cross-references: UNIPROT:Q929J2; GB:AL592022; PIDN:CAC97511.1; PID:g16414795; GSPDB:G  
A;Experimental source: strain Clipi1262  
C;Genetics:  
A;Gene: Lin2283

**Query**: Match 1 of 1  
**Match**: DKEZPd34F2322.1  
**Score**: 35.5%; **DB**: 2; **Length**: 49  
**Accession**: T42684  
**Submitted to**: the Protein Sequence Database, November 1994  
**Reference number**: Z22233  
**A;**  
**Accession**: T42684  
**A;**  
**Status**: preliminary  
**A;**  
**Molecule type**: mRNA  
**A;**  
**Residues**: 1-340 <AAA>  
**A;**  
**Cross-references**: UNIPROT:Q96W33; ENSEMBL:AU1334.05  
**A;**  
**Experimental source**: adult testis; clone DKEZPd434F2322.1  
**C;**  
**Genetics**:  
**A;**  
**Note**: DKEZPd34F2322.1

	Matches	Best Local Similarity	Locality	Query	Subject	Indels	Gaps
Oy	7	31.0%	10;	KIKITWKESETBEKULPVILAKQAL	RLSDVWRESLLEDQQLSPVLTPEHLL	Conservative	Mismatches
Db	297	31.0%	10;	:   :   :   :   :   :	:   :   :   :   :   :	Indels	Gaps

RESULT 9

RESULT 11  
B71480 probable agx-1 homolog-udp-glucose pyrophosphorylase - Chlamydia trachomatis (s

carboxyphosphonoenolpyruvate phosphomonomutase XFI234 [imported] - *Xylella fastidiosa* (str C;Species: *Xylella fastidiosa*)

C;Species: *Uromyces trachomatis*  
C;Date: 11-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004  
C;Accession: B140

C;Accession: B83707 C;Accession: B83707 #sequence-revision 20-Aug-2000 #text-change 09-JUL-2004  
R;anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen-  
Nature 405, 151-157, 2000  
A;Title: The genome sequence of the plant Pathogen *Xylella fastidiosa*.  
A;Reference number: A82517; Muid: 2030517; PMID:10910347  
A;Note: for a complete list of authors see reference number A53328 below

K; Stogmann, K.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Maratne, K.; Aravind, L.; Science 262, 754-759, 1998  
A; Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis  
A; Reference number: A71570; MURID:99000809; PMID:9784136  
A; Accession: B11480  
A; Status: preliminary  
A; Molecule type: DNA

A;Accession: B82707  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-298 <SIM>

A;Residues: 1-455 <ARN>  
A;Cross-references: UNIPROT:OB4720; GB:AE001342; GB:AE001273; NID:93329166; PID:

A; Cross-references: UNIPROT:Q9DZ4; GB:AB03957; GB:AE003849; NID:99106207; PIDN:AAF8404  
A; Experimental; strain: 9ASC  
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acebedo, M.; Alvarezga, R.; A  
Brienes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.R.A.; Carrasco, D.M.; Carrer, H  
as-Neto, R.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.;

A;Gene: C7715  
Query Match 35.5%; Score 49; DB 2; Length 455;  
Best Local Similarity 46.2%; Pred. No. 70;  
Matches 12; Conservative 6; Mismatches 8; Indels 0;  
Matches 12; Conservative 6; Mismatches 8; Indels 0;  
Gaps 0;

submitted to GenBank, June 2000.

QY 5 IKTTVIVESATEBKLTIVPULLAKOALJ 30  
Db :||: ; :||: :||: ; :||: 289  
264 IKTTLRSQAQEDVGVLJBLAKOKIAV

, P.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeira, D.A.; Rodrigues, V.; Rosa, A.J.C.; de Rosa Jr., V.E.; de Sa, R.G.; Sanejoli, R.V.; da Silveira, S.; Silva, A.; Authors; da Silva, A.C.R.; da Silva, F.R.; da Silva, M.; Tschalco, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A.; Reference number: A59328

RESULT 12  
IQBS44  
primosome component (helicase loader) dial - *Bacillus subtilis*  
N;Alternative names: dnaA protein homolog, 44K; hypothetical protein Y (dnab 3', rna

C;Species: *Bacillus subtilis*  
 C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004  
 C;Accession: B24720; C06580; F69617  
 R;Ogasawara, N.; Moriya, S.; Mazzola, P.G.; Yoshikawa, H.  
 Nucleic Acids Res. 14, 9989-9999, 1986  
 A;Reference number: A93650; MUID:87117549; PMID:3027671  
 A;Accession: B24720  
 A;Molecule type: DNA  
 A;Residues: 1-311 <OGA>  
 A;Cross-references: UNIPROT:P06567; GB:X04963; NID:939880; PIDN:CAA28633.1; PID:939881  
 R;Hoshino, T.; McKenzie, T.; Schmidt, S.; Tanaka, T.; Sueoka, N.  
 A;Title: Nucleotide sequence of *Bacillus subtilis* dnaB: a gene essential for DNA replica  
 A;Reference number: A94709; MUID:87118226; PMID:3027697  
 A;Accession: C026580  
 A;Molecule type: DNA  
 A;Residues: 1-18, N'-20-23, 'T', 25-206 <HOS>  
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertet  
 C.; Brion, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc  
 A.; D'Urbil, S.; Emmerson, P.T.; Entian, J.; Fabret, C.; Ferrari, B.  
 Nature 390, 249-255, 1997  
 A;Authors: Fouger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler  
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hollsappel, S.; Hullo, M.P.;  
 Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
 A.; Antibus, J.; Laufer, J.; Lazarevic, V.; Lee, S.M.; Levin, A.; Liu, H.; Masuda, S.; Mauveel  
 Y.; M.; Ogasawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porteille  
 Rieger, M.; Rivolta, C.; Rocha, S.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon  
 A;Authors: Schleich, S.; Schroeter, R.; Scifoone, F.; Sekiguchi, J.; Sekowska, A.; Seror,  
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Togomi, A.; Tosato, V.; Uchiyama,  
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
 A;Authors: Yoshikawa, H.F.; Zumstein, B.; Yoshikawa, H.; Danchin, A.  
 A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
 A;Reference number: A65980; MUID:9844033; PMID:9384377  
 A;Accession: F6617  
 A;Residues: 1-311 <KUN>  
 A;Molecule type: DNA  
 A;Cross-references: GB:939118; GB:AL009126; NID:92635200; PIDN:CAB14858.1; PID:92635363  
 A;Experimental source: strain 168  
 C;Genetics:  
 A;Gene: dnaI  
 C;Superfamily: 44K dnaA Protein homolog  
 C;Keywords: ATP; nucleotide binding; P-loop  
 F;168-175/Region: nucleotide-binding motif A (P-loop)

Query Match 35.1%; Score 48.5%; DB 1; Length 311;  
 Best Local Similarity 33.3%; Pred. No. 54;  
 Matches 11; Conservative 8; Mismatches 9; Indels 5; Gaps 1;

Qy	2 VEKIKTVKESATEEKL-----TPVILAKQIAA 29
Db	201 VRELKNSLQDQTLBEEKLMVYKTPVLMDDIGA 233

RESULT 13  
 T52331 hypothetical protein ZCF37 [imported] - *Arabidopsis thaliana*  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Date: 24-Oct-2000 #sequence\_revision 24-Oct-2000 #text\_change 09-Jul-2004  
 C;Accession: T52431  
 R;Kato, A.; Suzuki, M.; Kuwahara, A.; Ooe, H.; Higano-Inaba, K.; Komeda, Y.  
 Gene 239, 309-3116, 1999  
 A;Title: Isolation and analysis of cDNA within a 300 kb *Arabidopsis thaliana* genomic region  
 A;Reference number: 225171  
 A;Accession: T52431  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-211 <KAT>  
 A;Cross-references: UNIPROT:Q9SLT9; EMBL:AB028229; PIDN:BAA87954.1  
 A;Experimental source: cultivar Columbia  
 C;Genetics:  
 A;Map position: 1

A;Note: ZCF37.  
 Query Match 34.8%; Score 48; DB 2; Length 211;  
 Best Local Similarity 64.3%; Pred. No. 42; 2; Indels 0; Gaps 0;  
 Matches 9; Conservative 3; Mismatches 2;  
 Qy 3 EKIKTVKESATEE 16  
 Db 91 DKVKTEVKETEE 104

RESULT 14  
 T34100 hypothetical protein C17G10.2 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T34100  
 A;Molecule type: DNA  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Gene: CESP:C17G10.2  
 A;Accession: C17G10.2  
 A;Map position: 2  
 A;Introns: 3/6/3; 81/1; 167/1; 232/3; 355/3  
 Query Match 34.8%; Score 48; DB 2; Length 379;  
 Best Local Similarity 32.1%; Pred. No. 79;  
 Matches 9; Conservative 9; Mismatches 10; Indels 0; Gaps 0;  
 Qy 2 VEKIKTVKESATEEKL-----TPVILAKQIAA 29  
 Db 75 IEALQASIKNSPDRLKNAVLYFNRAA 102

RESULT 15  
 D75056 cell division control protein. PAB2373 - *Pyrococcus abyssi* (strain Orsay)  
 C;Species: *Pyrococcus abyssi*  
 C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
 C;Accession: D75056  
 R;anonymous, Genoscope submitted to the EMBL Data Library, July 1999  
 A;Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome structure  
 A;Reference number: A75001  
 A;Accession: D75056  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-1112 <KAW>  
 A;Cross-references: UNIPROT:Q9URR7; GB:AJ248287; GB:AL096836; NID:95458657; PIDN:CAB5034  
 A;Experimental source: strain Orsay  
 C;Genetics:  
 A;Gene: cdc21; PAB2373  
 Query Match 34.8%; Score 48; DB 2; Length 1112;  
 Best Local Similarity 40.0%; Pred. No. 2.5e+02; 4; Indels 6; Gaps 3;  
 Matches 14; Conservative 11; Mismatches 4;  
 A;Reference number: 225171  
 A;Accession: T52431  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-211 <KAT>  
 A;Cross-references: UNIPROT:Q9SLT9; EMBL:AB028229; PIDN:BAA87954.1  
 A;Experimental source: cultivar Columbia  
 C;Genetics:  
 A;Map position: 1

Search completed: November 3, 2005, 22:04:14  
 Job time : 11.9091 secs

GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: November 3, 2005, 21:37:29 ; Search time 91.4866 Seconds

(without alignments)  
 291.060 Million cell updates/sec

Title: 09782816-51

Perfect score: 251

Sequence: 1 GVKETPQQKYQYORLHLHSVQEL.....ESATEEKLTVPVLAQQLAAL 52

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03; \*

1: uniprot\_sprot; \*

2: uniprot\_trembl; \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score % Query Match Length DB ID Description

Result No.	Score	%	Query	Match	Length	DB	ID	Description
1	251	100.0	400	1	DCT2_HUMAN		Q13361	homo sapien
2	248	98.8	401	1	DCT2_MOUSE		Q9K18	mus musculus
3	248	98.8	402	2	Q6AYH5		Q6ayh5	rattus norvegicus
4	220	87.6	403	2	Q61RB3		Q61rb3	xenopus laevis
5	213	84.9	403	2	Q66J30		Q66j30	xenopus laevis
6	211	84.1	338	2	Q7ZXY2		Q7zxy2	xenopus laevis
7	177	70.5	402	2	Q9PTG6		Q9ptg6	zebrafish
8	177	70.5	405	2	Q7T3H1		Q7t3h1	brachydanio
9	76	30.3	402	2	Q6IP53		Q6ip53	xenopus laevis
10	72.5	28.9	380	2	Q9V4Y9		Q9v4y9	drosophila
11	71	28.3	800	2	Q6MVPT		Q6mvpt	neurospora
12	71	28.3	813	2	Q7SH14		Q7sh14	neurospora
13	70	27.9	311	2	Q97IV5		Q97iv5	sulfobolus
14	70	27.9	751	2	Q8MQK1		Q8mqk1	drosophila
15	70	27.9	1087	2	Q86BSS		Q86bss	drosophila
16	70	27.9	1124	2	Q8M0Q2		Q8m0q2	drosophila
17	70	27.9	2199	2	Q7PUP2		Q7pup2	ampheltes
18	69.9	27.7	873	2	Q95X56		Q95x56	caenorhabditis
19	69.5	27.7	919	2	Q95X55		Q95x55	caenorhabditis
20	68	27.1	1755	2	Q7RV31		Q7rv31	neurospora
21	68	27.1	1968	2	Q8X0C5		Q8x0c5	neurospora
22	67.5	26.9	1868	2	Q6BNV2		Q6bnv2	deoxyribose
23	67	26.7	455	2	Q7ZVF1		Q7zvf1	brachydanio
24	67	26.7	639	2	Q7ZVF1		Q7zvf1	brachydanio
25	67	26.7	1795	2	Q9LJC9		Q9ljc9	caenorhabditis
26	67	26.7	2478	2	Q9LCH2		Q9lch2	staphylococci
27	67	26.7	2478	2	Q9RL69		Q9rl69	staphylococci
28	67	26.7	2481	2	Q99QR6		Q99qr6	staphylococci
29	67	26.7	2481	2	Q7A4B1		Q7a4b1	staphylococci
30	66	26.3	393	2	Q49567		Q49567	arabidopsis
31	66	26.3	860	2	Q7Q0Q9		Q7q0q9	anopheles

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03; \*

1: uniprot\_sprot; \*

2: uniprot\_trembl; \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RA Echeverri C.J., Paechter B.M., Vaughan K.T., Vallee R.B.;

RT "Molecular characterization of the 50-kDa subunit of dynein reveals

RT function for the complexin in chromosome alignment and spindle

RT organization during mitosis".

J. Cell Biol. 132:617-633(1996).

[2] SEQUENCE FROM N.A.

RC TISSUE=Placenta, Skin, and Uterus;

RX MEDLINE=2238887; PubMed=1247973; DOI=10.1073/pnas.242603899;

RA Strauberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Butet K.H., Schaefer C.P., Blat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schatz T.E.,

RA Brownstein M.J., Udin T.B., Yoshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loucellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McElroy P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fehay J., Heitton E., Keightman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grinberg J., Schmutz J., Myers R.M., Smalius D.E.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,

RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[3] SEQUENCE OF 1-384 FROM N.A.

RP Aumanis J.P., Yu-Lee L.-Y.;

RT "Human 50 kD dynein subunit, p50 dyneinin, isolated from Hela

cells";

RT Submitted (NOV-2002) to the EMBL/GenBank/DDJB databases.

[4] SEQUENCE OF 1-13.

084500	chlamydia t
Q8tb98	homo sapien
074424	schizosaccharomyces pombe
Q7pz25	anopheles gambiae
Q8li19	oryza sativa
Q9bz3	homo sapien
Q9um00	homo sapien
Q92113	mus musculus
Q6dgw9	brachydanio
Q8iy3	arabidopsis thaliana
Q7545	homo sapien
Q9qf1	drosophila melanogaster
Q9y2k3	homo sapien
P51714	bacteriophage lambda

RC TISSUE=Platelet; PubMed=12665801; DOI=10.1038/nbt810;  
 RX MEDLINE=22608398; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Gevertz K., Goethals M., Martens L., Van Damme J., Staes A.,  
 RA Thomas G.R., Vandekerckhove J.;  
 RT "Exploring proteomes and analyzing protein processing by mass  
 RT spectrometric identification of sorted N-terminal peptides";  
 RL Nat. Biotechnol. 21: 566-569(2003).  
 CC -!- FUNCTION: Modulates cytoplasmic dynein binding to an organelle,  
 CC and plays a role in prometaphase chromosome alignment and spindle  
 CC organization during mitosis. May play a role in synapse formation  
 CC during brain development.  
 CC -!- SUBUNIT: Subunit of dynein, a multiprotein complex associated  
 CC with dynein.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.  
 CC  
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 CC  
 DR EMBL; U507033; AAC0423.1; -.  
 DR BC000718; AAC00718.1; -.  
 DR EMBL; BC009468; AAH09468.1; -.  
 DR EMBL; BC014083; AAH14083.1; -.  
 DR EMBL; AY189155; AAC034395.1; -.  
 DR Genew; HGNC:2112; DCTN2.  
 RN MIN; 60776; -.  
 DR GO; GO:0005813; C:centrosome; TAS.  
 DR GO; GO:0005869; C:dynein complex; TAS.  
 DR GO; GO:0000776; C:kinetochore; TAS.  
 DR GO; GO:0008283; P:cell proliferation; TAS.  
 DR GO; GO:007067; :mitosis; TAS.  
 DR InterPro; IPR06996; Dynamitin.  
 DR Pfam; PF04912; Dynamitin: 1.  
 KW Coiled coil; Cytoskeleton; Direct protein sequencing; Dynein;  
 KW Membrane; Microtubule; Motor protein.  
 FT INIT\_MET 0  
 FT DOMAIN 98 131 Coiled coil (Potential).  
 FT DOMAIN 213 243 Coiled coil (Potential).  
 FT DOMAIN 378 398 Coiled coil (Potential).  
 FT CONFLICT 34 34 A -> AFAQEL (in Ref. 1).  
 FT CONFLICT 35 35 E -> ELE (in Ref. 3).  
 FT CONFLICT 381 384 LATV -> PGHS (in Ref. 3).  
 SQ SEQUENCE 400 AA; 44099 MW; OA95AE95COBB270F CRC64;  
 Query Match Best Local Similarity 100.0%; Score 251; DB 1; Length 400;  
 Matches 52; Conservative 0; MisMatches 0; Indels 0; Gaps 0;  
 Qy 1 GVKERPPQQKQYRQLHLHQELTEVEKIKTTKESATEKUTPVLLAKQALN 52  
 Db 93 GVKERPPQQKQYRQLHLHQELTEVEKIKTTKESATEKUTPVLLAKQALN 144  
 RESULT 2  
 DCT2\_MOUSE STANDARD PRT; 401 AA.  
 ID DCT2\_MOUSE  
 AC Q99KU8;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 05-TUL-2004 (Rel. 44, Last annotation update)  
 DE Dynactin complex 50 kDa subunit (50 kDa dynein-associated polypeptide)  
 DE (p50 dynamin) (DCTN-50) (Dynactin 2) (Growth cone membrane protein  
 DE 23-88K) (CNP23-48K).  
 Name=Dctn2;  
 OS Mus musculus (Mouse);  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10050;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Kleinber R.D., Collins F.S., Wagner J.J., Sherman C.M., Schuler G.D.,  
 RA Altshull S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Blat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.B.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullany S.J.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Boksa S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Farney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J.J., Schmutz J.J., Myers R.M.,  
 RA Butterfield Y.S.N., Krywawiksi M.I., Skalaka U., Smilus D.E.,  
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16839-16903 (2002).  
 RN [2]  
 RP SEQUENCE OF 65-74; 77-91; 102-116; 156-170; 194-216 AND 309-320;  
 RP SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
 RN [3]  
 RP INTERACTION WITH BICD2.  
 RX MEDLINE=21376052; PubMed=11483508; DOI=10.1093/emboj/20.15.4041;  
 RA Hoogenraad C.C., Akhmanova A., Howell S.A., Dorfland B.R.,  
 RA de Zeeuw C.I., Willmesen R., Visser P., Grosveld F., Gallart N.,  
 RT "Mammalian Golgi-associated Bicaudal-D2 functions in the dynein-  
 RT dynein pathway by interacting with these complexes.";  
 RL 20:4041-4054 (2001).  
 CC -!- FUNCTION: Modulates cytoplasmic dynein binding to an organelle,  
 CC and plays a role in prometaphase chromosome alignment and spindle  
 CC organization during mitosis. May play a role in synapse formation  
 CC during brain development.  
 CC -!- SUBUNIT: Subunit of dynein, a multiprotein complex associated  
 CC with dynein (By similarity). Interacts with BICD2.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.  
 CC -!- DEVELOPMENTAL STAGE: Present at high levels in both cytoplasmic  
 CC and membrane-associated forms in neonates. Levels of membrane-  
 CC associated form are greatly reduced in the adult.  
 CC  
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 CC  
 DR EMBL; BC004613; AAH04613.1; -.  
 DR MGD; MGI:107733; Dctn2.  
 DR InterPro; IPR06996; Dynamitin.  
 DR Pfam; PF04912; Dynamitin; 1.  
 KW Coiled coil; Cytoskeleton; Direct protein sequencing; Dynein;  
 KW Membrane; Microtubule; Motor protein.  
 FT INIT\_MET 0  
 FT DOMAIN 98 131 By similarity.  
 FT DOMAIN 214 244 Coiled coil (Potential).  
 SQ SEQUENCE 401 AA; 43385 MW; 1535EA4ABD5940BC CRC64;  
 Query Match Best Local Similarity 98.8%; Score 248; DB 1; Length 401;  
 Matches 51; Conservative 1; MisMatches 0; Indels 0; Gaps 0;

RESULT 3		1 GVKETPQQKQYORLHLHVOELTEVEKIKITWESATEEKLTTPVLLAKQAL 52
ID Q6AYH5	PRELIMINARY;	PRT; 402 AA.
AC Q6AYH5;		DT 25-OCT-2004 (TREMBREL. 28, Created)
DT 25-OCT-2004 (TREMBREL. 28, Last sequence update)		DT 25-OCT-2004 (TREMBREL. 28, Last annotation update)
DE Dynactin 2.		DE Dynactin 2.
GN Name=Dcn2;		OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.		OC
OX NCBI_TaxID=8355;		RN [1]
RP SEQUENCE FROM N.A.		RC TISSUE=Embryo;
RC PubMed=12477312; DOI=10.1073/pnas.242603899;		RX MEDLINE=22388257; PubMed=12477312; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,		RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,		RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA Blatchko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,		RA Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,
RA brownstein M.J., Usdin T.B., Toshiyuki S., Garnicini P., Prange C.,		RA Brownstein M.J., Usdin T.B., Toshiyuki S., Garnicini P., Prange C.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,		RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Gunaratne P.H.,		RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,		RA Blakeley R.W., Touchman J.W., Green E.P., Dickson M.C.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		RA Jones S.J., Marra M.A.;
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,		"Generation and initial analysis of more than 15,000 full-length human
RA Jones S.J., Marra M.A.;		RT and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RT "Generation and initial analysis of more than 15,000 full-length human		RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RT and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		RT [2]
RN TISSUE=Testis;		RC TISSUE=Embryo;
RC Director MGC Project;		RX MEDLINE=22341132; PubMed=1245917; DOI=10.1002/dvdy.10174;
RL Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.		RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
DR EMBL; GO:0005869; C:dynatin complex; IEA.		RA Richardson P.;
DR GO; GO:0007017; P:microtubule-based process; IEA.		DR "Genetic and genomic tools for Xenopus research: The NIH Xenopus
DR InterPro; IPR006996; Dynamitin.		DR initiative"; Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		DR Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RT Dev. Dyn. 225:384-391(2002).		DR Jones S.J., Marra M.A.;
RN [3]		RL TISSUE=Embryo;
RP TISSUE=Testis;		RX MEDLINE=22341132; PubMed=1245917; DOI=10.1002/dvdy.10174;
RC Director MGC Project;		RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RL Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.		RA Richardson P.;
DR EMBL; BC010987; AAH0987_1; -.		DR "Genetic and genomic tools for Xenopus research: The NIH Xenopus
DR GO; GO:0005869; C:dynatin complex; IEA.		DR initiative"; Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
DR GO; GO:0007017; P:microtubule-based process; IEA.		DR Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
DR InterPro; IPR006996; Dynamitin.		DR Jones S.J., Marra M.A.;
SQ SEQUENCE 402 AA; 44148 MW; 550335535A4FB052 CRC64;		RL Dev. Dyn. 225:384-391(2002).
Query Match 98.8%; Score 248; DB 2; Length 402; Best Local Similarity 98.1%; Pred No. 9.4e-17; Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	QY 1 GVKETPQQKQYORLHLHVOELTEVEKIKITWESATEEKLTTPVLLAKQAL 52	RN [1]
QY 1 GVKETPQQKQYORLHLHVOELTEVEKIKITWESATEEKLTTPVLLAKQAL 52	QY 1 GVKETPQQKQYORLHLHVOELTEVEKIKITWESATEEKLTTPVLLAKQAL 52	RESULT 5
Db 94 GVKETPQQKQYORLHLHVOELTEVEKIKITWESATEEKLTTPVLLAKQAL 145	Db 94 GVKETPQQKQYORLHLHVOELTEVEKIKITWESATEEKLTTPVLLAKQAL 145	Q66JJ0 PRELIMINARY; PRT; 403 AA.
RESULT 4		Q66JJ0 PRELIMINARY; PRT; 403 AA.
ID Q6IRB3	PRELIMINARY;	AC 066JJ0
ID Q6IRB3;	PRT;	AC 066JJ0
AC Q6IRB3;		AC 066JJ0
DT 05-JUL-2004 (TREMBREL. 27, Created)		DT 25-OCT-2004 (TREMBREL. 28, Created)
DT 05-JUL-2004 (TREMBREL. 27, Last sequence update)		DT 25-OCT-2004 (TREMBREL. 28, Last sequence update)
DT 05-JUL-2004 (TREMBREL. 27, Last annotation update)		DT 25-OCT-2004 (TREMBREL. 28, Last annotation update)
DE Dctn2-prov protein.		DR MGCB122 protein;
DE Dctn2-prov protein.		DR MGCB122;
GN Name=dctn2-prov;		GN Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).		OS Xenopus laevis (African clawed frog).
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
		OC Xenopodinae; Xenopus.
		OX NCBI_TaxID=8355;
		RN [1]



DR	GO; GO:0007017; P:microtubule-based process; IEA.
DR	InterPro; IPR006986; Dynamitin.
DR	Pfam; PF04912; Dynamitin_1.
SQ	SEQUENCE 402 AA; 45126 MW; F229C467C630DCB9 CRC64;
Query Match	Best Local Similarity 70.5%; Score 177; DB 2; Length 402; Matches 35; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
QY	1 GVKEPPOQKYQRLHEVOLTEVEKIKTVKESATEEKLTPTVLAKOALAL 52
Db	96 GVKETPQQKYQRLHEVOLTEVEKIKTVKESATEEKLTPTVLAKOALAL 52
RESULT 8	
Q7N3H1	PRELIMINARY; PRT; 405 AA.
ID	Q7N3H1
AC	Q7N3H1; PRELIMINARY; PRT; 405 AA.
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	Similar to dynactin 2 (P50).
GN	ORFNames-zgc:63867;
OS	Brachydanio rerio (Zebrafish) (Danio rerio).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
OC	NCBI_TaxID=7955;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;
RX	MEDLINE:22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Degege J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Matsushita K., Farmer A.P., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pange C., Raha S.S., Loquelandano N.A., Peters G.J., Abramson R.D., Millahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murry D.M., Soderren E.J., Lu X., Gibbs R.A., Fahey J., Heiton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko E.D., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.B., Schnurch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;
RX	MEDLINE:22341132; PubMed=12454917; DOI=10.1002/qdy.10174;
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.
RA	"Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative"; Dev. Dyn. 225:384-391(2002).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;
RA	Klein S., Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC053120; AAH53120.1; -.
DR	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC053120; AAH53120.1; -.
DR	ZFIN; ZDB-GENE-0426-1279; zgc:63867;
DR	GO; GO:0005889; C:dynamic complex; IEA.
DR	GO; GO:0007017; P:microtubule-based process; IEA.
DR	InterPro; IPR006986; Dynamitin.
DR	Pfam; PF04912; Dynamitin_1.
SQ	SEQUENCE 405 AA; 44625 MW; CA00047342500953 CRC64;
Query Match	Best Local Similarity 70.5%; Score 177; DB 2; Length 405; Matches 35; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
QY	1 GVKEPPOQKYQRLHEVOLTEVEKIKTVKESATEEKLTPTVLAKOALAL 52
Db	96 GVKETPQQKYQRLHEVOLTEVEKIKTVKESATEEKLTPTVLAKOALAL 52
RESULT 9	
Q9V4Y9	PRELIMINARY; PRT; 380 AA.
ID	Q9V4Y9

- AC Q9V4Y9; DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE CG8269-PA (L007994);  
 GN Name=Dmr; ORFNames=CG8269;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Mecomorpha;  
 OC Ephydrioidea; Drosophilidae; Drosophila;  
 RN NCBI\_TaxID=7227;
- RN SEQUENCE FROM N.A.  
 RX MEDLINE:20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Goeayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortsman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Change M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Heitl G., Nelson C.R., Gabor G.I.,  
 RA Abril J.P., Agbayani A., An H.J., Andersen-Sampathkoch C., Baldwin D.,  
 RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,  
 RA Beeson K.Y., Benos P.V., Belmont B.P., Bhambhani D., Bolshakov S.,  
 RA Borckova D., Botchan M.R., Bouck J., Brokstein P., Brottner P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu B., Centner A., Chandra I.,  
 RA Cherry J.M., Cowley S., Dahake C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Geng F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hottin D., Houston K.A., Howland T.J., Wei M.H., Ibeewam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.B., Kodira C.D., Kraft C.A., Krawitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milashina N.V., Mobarry C., Morris J., Mohrefi A.,  
 RA Mount S.M., Moy M., Murphy C., Murphy L., Mizny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,  
 RA Palazzolo M., Pittman G.S., Paud S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington J., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Klamo I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter C., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodage R., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*";  
 RL Science 287:2185-2195(2000).
- [1] SEQUENCE FROM N.A.  
 RX MEDLINE:22426065; PubMed=12537568;  
 RA Celinker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champé M., Dugan S.P., Frise E., Hodgson A.,  
 RA George R.A., Hoskins R.A., Hawerty T., Muñoz D.M., Nelson C.R.,  
 RA Pasch J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstock G., Scheerer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
 RT "Finishing a whole genome shotgun: Release 3 of the *Drosophila*  
 melanogaster euchromatic genome sequence";  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
- RN SEQUENCE FROM N.A.  
 RX MEDLINE:22426065; PubMed=12537573;  
 RA Celinker S.E., Bergman C.M., Kronmiller B., Carlson J., Svirska R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celinker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 a genomic perspective";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
- [4] SEQUENCE FROM N.A.  
 RX MEDLINE:22426072; PubMed=12537572;  
 RA Misra S., Crosey M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
 RA Smith C.D., Tupy J.L., Whited E.J., Bayraktaroglu L., Bernink B.P.,  
 RA Bettencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 systematic review";  
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
- [5] SEQUENCE FROM N.A.  
 RX MEDLINE:22426073; PubMed=12537573;  
 RA Flibase;  
 RG Submitted (SEP-2002) to the EMBL/GenBank/DDJB databases.
- [6] SEQUENCE FROM N.A.  
 RX Flibase;  
 RG Submitted (MAR-2004) to the EMBL/GenBank/DDJB databases.
- [7] SEQUENCE FROM N.A.  
 RX STRAIN=berkeley;  
 RC SEQUENCE FROM N.A.  
 DR Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Chang'e M., Chavez C., Dorsett V., Farrián D., Frisse E., George R.,  
 RA Gonzalez M., Guarín H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nunoo J., Paclob J., Paraga V., Park S., Phouanenavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celinker S.,  
 RA Submitted (OCT-2001) to the EMBL/GenBank/DDJB databases.  
 DR EMBL; AE003835; AAF59034.1; .  
 DR EMBL; AY061092; AAI28640.1; .  
 DR INACTA; Q9V4Y9; .  
 DR FlyBase; FBgn0021025; Dmn.  
 DR GO; GO:0005865; C:dynatin complex; IEA.  
 DR GO; GO:0007017; P:microtubule-based process; IEA.  
 DR InterPro; IPR006996; Dynamitin.  
 DR Pfam; PF04912; Dynamitin\_1.  
 SQ SEQUENCE 380 AA; 41998 MW; CF7E1D3BFF5989C5 CRC64;
- Query Match 28.9%; Score 72.5%; DB 2; Length 380;  
 Best Local Similarity 48.7%; Pred. No. 34;  
 Matches 19; Conservative 5; Mismatches 14; Indels 1; Gaps 1;  
 QY 1 GVKEPDKQKYQRLHAEVQSLTTVEVKITKTVKESATEEK 39  
 DB 94 GEKETPVKQQLQIEMELLINEVAQVD-RKVADEEK 131
- RESULT 11  
 Q6MVP7  
 ID Q6MVP7  
 AC Q6MVP7;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DE Probable translation elongation factor EF-G, mitochondrial.  
 GN Name=B16018.090;  
 OS Neurospora crassa.  
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 CC Sordariomycotina; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 RX NCBI\_TaxID=5141;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DDJB databases.
- [1] SEQUENCE FROM N.A.  
 RA Schulte U., Aign V., Hoheisel J., Brandt P., Partmann B., Holland R.,  
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DDJB databases.
- [2] SEQUENCE FROM N.A.  
 RA German Neurospora genome project;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DDJB databases.  
 DR EMBL; BX42625; CAB37629.1; .  
 GO; GO:0005525; F:GTP binding; IEA.

DR	GO; GO:0003746; F:translation elongation factor activity; IEA.	DR	GO; GO:0003746; F:translation elongation factor activity; IEA.
DR	GO; GO:0006412; P:protein biosynthesis; IEA.	DR	GO; GO:0006412; P:protein biosynthesis; IEA.
DR	GO; GO:0006414; P:translational elongation; IEA.	DR	GO; GO:0006414; P:translational elongation; IEA.
DR	InterPro; IPR004540; EF-G.	DR	InterPro; IPR004540; EF-G.
DR	InterPro; IPR000640; EFG-C.	DR	InterPro; IPR000640; EFG-C.
DR	InterPro; IPR009022; EFG-III_V.	DR	InterPro; IPR009022; EFG-III_V.
DR	InterPro; IPR005517; EFG-IV.	DR	InterPro; IPR005517; EFG-IV.
DR	InterPro; IPR004161; EFTU_D2.	DR	InterPro; IPR004161; EFTU_D2.
DR	InterPro; IPR002795; ProtSyn_GTPbind.	DR	InterPro; IPR002795; ProtSyn_GTPbind.
DR	InterPro; IPR005225; Small_GTP.	DR	InterPro; IPR005225; Small_GTP.
DR	InterPro; IPR009000; TransfT_factor.	DR	InterPro; IPR009000; TransfT_factor.
DR	Pfam; PF00679; EFG_C; 1.	DR	Pfam; PF00679; EFG_C; 1.
DR	Pfam; PF03764; EFG_IV; 1.	DR	Pfam; PF03764; EFG_IV; 1.
DR	Pfam; PF00009; GTP_EFTU; 1.	DR	Pfam; PF00009; GTP_EFTU; 1.
DR	Pfam; PF03144; GTP_EFTU_D2; 1.	DR	Pfam; PF03144; GTP_EFTU_D2; 1.
DR	PRINTS; PR00315; ELONGATNFCT.	DR	PRINTS; PR00315; ELONGATNFCT.
DR	TIGRFAMS; TIGR0044; EF-G; 1.	DR	TIGRFAMS; TIGR0044; EF-G; 1.
DR	TIGRFAMS; TIGR00231; small_GTP; 1.	DR	TIGRFAMS; TIGR00231; small_GTP; 1.
DR	PROSITE; PS00301; EFACTOR_GTP; 1.	DR	PROSITE; PS00301; EFACTOR_GTP; 1.
KW	Elongation_factor; GTP-binding; Protein biosynthesis.	KW	GTP-binding; Hypothetical_protein; Protein biosynthesis.
SQ	SEQUENCE 800 AA; 88373 MW; F2A7C425FD4974A CRC64;	SQ	SEQUENCE 813 AA; 89810 MW; CGA503F35B29B05 CRC64;
<b>RESULT 12</b>			
Q7SH14	PRELIMINARY; PRT; 813 AA.	Q7SH14	PRELIMINARY; PRT; 813 AA.
AC	Q7SH14; 01-MAR-2004 (Tremblrel. 26, Created)	AC	Q7SH14; 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)	DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE	Hypothetical protein.	DE	Hypothetical protein.
GN	Name=NCUT02955_1;	GN	Name=NCUT02955_1;
OS	Neurospora crassa.	OS	Neurospora crassa.
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;	OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC	Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.	OC	Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX	NCBI_TaxID=5141;	OX	NCBI_TaxID=5141;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	STRAIN=OR74A;	RC	STRAIN=ICM 10545 / 7;
RA	Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Ellis D., Engels R., Wang S., Nielsen C.B., Butler J., Edström M., Choi D., Ianakiev P., Pedersen D., Nelson M., Washburn M., Seitzeminkoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Rothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Nayler J., Thomann N., Barrett R., Gnerre S., Kanal M., Kauvayseleis M., Muccielli E., Bielke C., Rudd S., Friedman D., Kystofova S., Rasmussen C., Matzenberg R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catcheseide D., Li W., Pratt R.J., Osman S.A., Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarde A., Plaman M., Seller S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen T., Sachs M.S., Lander E.S., Nusbaum C., Birren B., RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.", Nature 0:0-0(2003).	RA	Strain=ICM 10545 / 7; MEDLINE=11572479; Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anka A., Kosugi H., Hosoya A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanggi M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.; "Complete genome sequence of an aerobic thermosacidophilic bacterium, Sulfolobus tokodaii strain7."; Crenarchaeon, Sulfolobus tokodaii strain7.; DNA Res. 8:23-140(2001). DR EMBL; AP000885; BAB66315_1; -. HSSP; P0110; IPI05. Complete proteome; Hypothetical protein.
RL	Nature 0:0-0(2003).	RL	Query Match Best Local Similarity 27.9%; Score 70; DB 2; Length 311; Matches 18; Conservative 11; Mismatches 18; Indels 4; Gaps 2; DR EMBL; ABX0100006; EAA36106_1; -. HSSP; P13551; 1FNM. GO; GO:0005525; P:GTP binding; IEA.
CC	-1 - CAUTION: The sequence shown here is derived from an preliminary data.	CC	EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
DR	DR	DR	DR

RESULT 14  
 QBNOKI; PRELIMINARY; PRT; 751 AA.  
 ID QBNOKI; PRELIMINARY; PRT; 751 AA.  
 DT 01-OCT-2002 (TREMBLel. 22, Created)  
 DT 01-OCT-2002 (TREMBLel. 22, Last sequence update)  
 DT 01-MAR-2004 (TREMBLel. 26, Last annotation update)  
 DB LD08185P;  
 GN ORFNames=CG10971;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Epiphydroidea; Drosophilidae; Drosophila;  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=berkeley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Carlson J., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W., Fosler C., Gabriel A.E., Garg N.S., Geibart W.M., Glaser K., Globek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Houston K.A., Holman T.J., Weintraub H., Ibeagwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitt A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M., McPherson D., Merrilov G., Milashina N.V., Mobarry C., Morris J., Moskrai A., Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Pacileo J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D., Scheer P., Shen H., Shue B.C., Siden-Kiamoo I., Simpson M., Stupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Swirskas R., Tector C., Turner E., Vanter E., Wang A.H., Wang X., Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.", Science 287:2185-2195(2000).  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AV1129439; AAH76181\_1; -.  
 DR FlyBase; FBgn0036309; CG10971;  
 DR InterPro; IPR02558; ILMQO.  
 DR Pfam; PF01608; I\_LMEO; 1.  
 DR PROSITE; PS50945; I\_LMEO; 1.  
 DR SEQUENCE; 751 AA; 85362 MW; 7EFBC7661CEBAA0 CRC64;  
 QY Best Local Similarity 27.9%; Score 70; DB 2; Length 751;  
 Matches 19; Conservative 9; Mismatches 11; Indels 4; Gaps 2;  
 RT  
 RESULT 15  
 Q8BS5 PRELIMINARY; PRT; 1087 AA.  
 AC Q8BS5; PRELIMINARY; PRT; 1087 AA.  
 DT 01-JUN-2003 (TREMBLel. 24, Created)  
 DT 01-JUN-2003 (TREMBLel. 24, Last sequence update)  
 DT 01-JUN-2004 (TREMBLel. 26, Last annotation update)  
 DE CG10971\_PB.  
 GN ORFNames=CG10971;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Epiphydroidea; Drosophilidae; Drosophila;  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RX MEDLINE-22426065; PubMed=12537568;  
 RX MEDLINE-22426070; PubMed=12537573;  
 RX MEDLINE-22426070; PubMed=12537573;  
 RN CELNIKER S.E., WHEELER D.A., KROMMILLER B., CARLSON J.W., HALPERN A., ADAMS M., CHAMPE M., DUGAN S.P., FRISE E., HODDISON A., GEORGE R.A., HOSKINS R.A., LAVERTY T., MUSNY D.M., NELSON C.R., PACLEB J.M., PARK S., PFEIFFER B.D., RICHARDS S., SODERGREN E.J., SVIRSKAS R., TABOR P.E., WAN K., STAPLETON M., SUTTON G.G., WEINSTOCK G., SCHERER S.E., MYERS E.W., GIBBS R.A., RUBIN G.M.; "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 RL SEQUENCE FROM N.A.  
 RN [3]  
 RP MEDLINE-22426070; PubMed=12537573;  
 RN CELNIKER S.J., BERGMAN C.M., KROMMILLER B., CARLSON J., SVIRSKAS R., PATEL S., FRISE E., WHEELER D.A., LEWIS S.E., ASHBURNER M., CELNIKER S.E.; "The transposable elements of the Drosophila melanogaster euchromatin: A genomics perspective.", Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE-22426069; PubMed=12537572;  
 RX MEDLINE-22426069; PubMed=12537572;  
 RA MISRA S., CROSBY M.A., MUNGALL C.J., MATTHEWS B.B., CAMPBELL K.S., RA HRADECKY P., HUANG Y., KAMINKER J.S., MILLBURN G.H., PROCCHNIK S.E., RA SMITH C.D., TUPY J.L., WHITFIELD C.J., BAYRAKTAROGLU L., BERMAN B.P., RA BETTCOURT B.R., CELNIKER S.E., DE GREY A.D., DRYSDALE R.A., RA HARRIS N.L., RICHIER J., RUSSO S., SCHROEDER A.J., SHU S.Q., RA STAPLETON M., YAMADA C., ASHBURNER M., GELBART W.M., RUBIN G.M., RA LEWIS S.E.; "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review", Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).  
 RL SEQUENCE FROM N.A.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RG FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RG FlyBase;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AE003540; ARF4984\_1; -.  
 DR FlyBase; FBgn0036309; CG10971;  
 DR GO; GO:0003779; F-actin binding; IEA.  
 DR GO; GO:0005543; F-Phospholipid binding; IEA.  
 DR InterPro; IPR01141; ANTH.  
 DR InterPro; IPR001026; Epsin\_N.

DR InterPro; IPR002558; ILWEO.  
DR InterPro; IPR008943; PI\_bind\_N.  
DR PF07651; ANTR; 1.  
DR PF01608; I\_LWEO; 1.  
DR Prodrom; P001820; ILWEO; 1.  
DR PROSITE; PS50942; ENTH; 1.  
DR PROSITE; PS50945; I\_LWEO; 1.  
SQ SEQUENCE 1087 AA; \_124298 MW; C83E709907DFFEBB CRC64;  
Query Match 27.9%; Score 70; DB 2; Length 1087;  
Best local Similarity 44.2%; Pred No. 1.8e-02;  
Matches 19; Conservative 9; Mismatches 11; Indels 4; Gaps 2;  
Qy 7 QKQYQRLHIVQEELTEVEKIKITVKESTEKEKUTPVLLAKQL 49  
Db 408 KQVNSQLLKETKELTNEISKIVNVEE--KEK-TNLILQKI 446  
Search completed: November 3, 2005, 22:03:04  
Job time : 91.4866 secs

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Gencore version 5.1.6  
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OM protein - protein search, using BW model  
 Run on: November 3, 2005, 21:51:39 ; Search time 26.6952 Seconds  
 (Without alignments)

145.410 Million cell updates/sec

Title: 09782816-51

Perfect score: 251

Sequence: 1 GVKERPPQKQYQRLLHEWQEL.....ESATEEKLTIVLAKQAL 52

Scoring table: BLOSUM62

Gappen 10.0 , Gapext: 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters:

513545

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents At: \*

1: /ccn2\_6/ptodata/1/1aa/5A-COMB.pep:\*

2: /ccn2\_6/ptodata/1/1aa/5B-COMB.pep:\*

3: /ccn2\_6/ptodata/1/1aa/6A-COMB.pep:\*

4: /ccn2\_6/ptodata/1/1aa/6B-COMB.pep:\*

5: /ccn2\_6/ptodata/1/1aa/pcTUS-COMB.pep:\*

/ccn2\_6/ptodata/1/1aa/backfillseqs1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	66	26.3	142	4	US-09-270-767-43370
2	64	25.7	639	4	US-09-513-992-540-14908
3	64	25.5	151	4	US-09-513-992-540-14908
4	64	25.5	193	4	US-09-107-53A-5587
5	63	25.1	850	4	US-09-269-858A-8
6	63	25.1	851	4	US-09-623-326-43
7	62.5	24.9	1270	4	US-09-538-092-1321
8	61.5	24.5	309	4	US-09-248-796A-14974
9	61.5	24.3	442	3	US-09-681-689-2
10	61	24.3	442	3	US-09-305-984-14
11	61	24.3	442	4	US-09-073-541A-14
12	61	24.3	442	4	US-09-493-940-14
13	61	24.3	442	4	US-09-583-110-5317
14	61	24.3	446	4	US-09-107-433-3720
15	61	24.3	644	1	US-08-487-890A-6
16	61	24.3	644	2	US-08-478-435-6
17	61	24.3	644	3	US-08-337-483-6
18	61	24.3	644	2	US-08-478-373-6
19	61	24.3	644	3	US-08-474-671-6
20	61	24.3	644	4	US-08-483-577A-6
21	61	24.3	644	3	US-08-897-438-6
22	61	24.3	644	3	US-08-637-654-6
23	61	24.3	644	3	US-08-649-518-5
24	60.5	24.1	87	3	US-09-284-033-3
25	60.5	24.1	1217	4	US-08-729-834B-3
26	60.5	24.1	1217	4	US-09-949-016-5454
27	59.5	23.7	424	4	US-09-286-981B-14

### ALIGNMENTS

Query	Match %	Length	DB ID	Description
QY	1	26.3%	US-09-270-767-43370	RESULT 1
QY	1	25.7%	US-09-513-992-540-14908	Sequence 43370, A
QY	1	25.5%	US-09-107-53A-5587	Sequence 7806, A
QY	1	25.5%	US-09-269-858A-8	Sequence 5587, APPLI
QY	1	25.1%	US-09-623-326-43	Sequence 8, APPLI
QY	1	24.9%	US-09-538-092-1321	Sequence 1321, APPLI
QY	1	24.5%	US-09-248-796A-14974	Sequence 14974, APPLI
QY	1	24.3%	US-09-681-689-2	Sequence 2, APPLI
QY	1	24.3%	US-09-305-984-14	Sequence 14, APPLI
QY	1	24.3%	US-09-073-541A-14	Sequence 14, APPLI
QY	1	24.3%	US-09-493-940-14	Sequence 14, APPLI
QY	1	24.3%	US-09-583-110-5317	Sequence 5317, APPLI
QY	1	24.3%	US-09-107-433-3720	Sequence 3720, APPLI
QY	1	24.3%	US-08-487-890A-6	Sequence 6, APPLI
QY	1	24.3%	US-08-478-435-6	Sequence 6, APPLI
QY	1	24.3%	US-08-337-483-6	Sequence 6, APPLI
QY	1	24.3%	US-08-478-373-6	Sequence 6, APPLI
QY	1	24.3%	US-08-474-671-6	Sequence 6, APPLI
QY	1	24.3%	US-08-483-577A-6	Sequence 6, APPLI
QY	1	24.3%	US-08-897-438-6	Sequence 6, APPLI
QY	1	24.3%	US-08-637-654-6	Sequence 6, APPLI
QY	1	24.3%	US-08-649-518-5	Sequence 6, APPLI
QY	1	24.1%	US-09-284-033-3	Sequence 3, APPLI
QY	1	24.1%	US-08-729-834B-3	Sequence 3, APPLI
QY	1	24.1%	US-09-949-016-5454	Sequence 4, APPLI
QY	1	23.7%	US-09-286-981B-14	Sequence 14, APPLI

Query	Match %	Length	DB ID	Description
QY	25.7%	25.5%	US-09-270-767-43370	RESULT 1
QY	25.5%	23.5%	US-09-513-992-540-14908	Sequence 43370, A
QY	25.5%	23.5%	US-09-107-53A-5587	Sequence 7806, A
QY	25.1%	23.5%	US-09-623-326-43	Sequence 8, APPLI
QY	24.9%	23.5%	US-09-538-092-1321	Sequence 1321, APPLI
QY	24.5%	23.5%	US-09-248-796A-14974	Sequence 14974, APPLI
QY	24.3%	23.5%	US-09-681-689-2	Sequence 2, APPLI
QY	24.3%	23.5%	US-09-305-984-14	Sequence 14, APPLI
QY	24.3%	23.5%	US-09-073-541A-14	Sequence 14, APPLI
QY	24.3%	23.5%	US-09-493-940-14	Sequence 14, APPLI
QY	24.3%	23.5%	US-09-583-110-5317	Sequence 5317, APPLI
QY	24.3%	23.5%	US-09-107-433-3720	Sequence 3720, APPLI
QY	24.3%	23.5%	US-08-487-890A-6	Sequence 6, APPLI
QY	24.3%	23.5%	US-08-478-435-6	Sequence 6, APPLI
QY	24.3%	23.5%	US-08-337-483-6	Sequence 6, APPLI
QY	24.3%	23.5%	US-08-478-373-6	Sequence 6, APPLI
QY	24.3%	23.5%	US-08-474-671-6	Sequence 6, APPLI
QY	24.3%	23.5%	US-08-483-577A-6	Sequence 6, APPLI
QY	24.3%	23.5%	US-08-897-438-6	Sequence 6, APPLI
QY	24.3%	23.5%	US-08-637-654-6	Sequence 6, APPLI
QY	24.3%	23.5%	US-08-649-518-5	Sequence 6, APPLI
QY	24.1%	23.5%	US-09-284-033-3	Sequence 3, APPLI
QY	24.1%	23.5%	US-08-729-834B-3	Sequence 3, APPLI
QY	24.1%	23.5%	US-09-949-016-5454	Sequence 4, APPLI
QY	23.7%	23.5%	US-09-286-981B-14	Sequence 14, APPLI





Query Match 24.3%; Score 61; DB 3; Length 442;  
 Best Local Similarity 33.3%; Pred. No. 23;  
 Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

QY 2 VKEPQQKYORL-----LHEVQLTTEVEKIKTVKESATEKLTTPVLLAKQL 49  
 Db 200 LIKEQINSLYQHLLTVIADLKNEALQLEKMKVFLRGASHELKTPLASKIL 253

RESULT 10  
 US-09-305-984-14  
 Sequence 14, Application US/09305984B  
 Patent No. 6331407  
 GENERAL INFORMATION:  
 APPLICANT: No. 6331407ak, Rodger  
 APPLICANT: Tounamen, Blaine  
 TITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME  
 FILE REFERENCE: 1340-1-016N1  
 CURRENT APPLICATION NUMBER: US/09/305, 984B  
 CURRENT FILING DATE: 1999-05-05  
 EARLIER APPLICATION NUMBER: 60/084, 399  
 EARLIER FILING DATE: 1998-05-06  
 EARLIER APPLICATION NUMBER: 09/305, 984  
 EARLIER FILING DATE: 1999-05-05  
 NUMBER OF SEQ ID NOS: 76  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 14  
 LENGTH: 442  
 TYPE: PRT  
 ORGANISM: Streptococcus pneumoniae  
 US-09-305-984-14

Query Match 24.3%; Score 61; DB 3; Length 442;  
 Best Local Similarity 33.3%; Pred. No. 23;  
 Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

QY 2 VKEPQQKYORL-----LHEVQLTTEVEKIKTVKESATEKLTTPVLLAKQL 49  
 Db 200 LIKEQINSLYQHLLTVIADLKNEALQLEKMKVFLRGASHELKTPLASKIL 253

RESULT 11  
 US-09-073-541A-14  
 Sequence 14, Application US/09073541A  
 Patent No. 6448224  
 GENERAL INFORMATION:  
 APPLICANT: No. 6448224ak, Rodger  
 APPLICANT: Tounamen, Elaine  
 TITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME  
 FILE REFERENCE: PAT000-07A  
 CURRENT APPLICATION NUMBER: US/09/583, 110  
 CURRENT FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: US 09/107, 433  
 PRIOR FILING DATE: 1998-06-30  
 PRIOR APPLICATION NUMBER: US 60/085, 131  
 PRIOR FILING DATE: 1998-05-12  
 PRIOR APPLICATION NUMBER: US 60/051, 553  
 PRIOR FILING DATE: 1997-07-02  
 NUMBER OF SEQ ID NOS: 5322  
 SEQ ID NO 5317  
 LENGTH: 442  
 TYPE: PRT  
 ORGANISM: Streptococcus pneumoniae  
 US-09-073-541A-14

Query Match 24.3%; Score 61; DB 4; Length 442;  
 Best Local Similarity 33.3%; Pred. No. 23;  
 Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

QY 2 VKEPQQKYORL-----LHEVQLTTEVEKIKTVKESATEKLTTPVLLAKQL 49  
 Db 200 LIKEQINSLYQHLLTVIADLKNEALQLEKMKVFLRGASHELKTPLASKIL 253

RESULT 12  
 US-09-492-940-14  
 Sequence 14, Application US/09493940

Query Match 24.3%; Score 61; DB 4; Length 442;  
 Best Local Similarity 33.3%; Pred. No. 23;  
 Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

QY 2 VKEPQQKYORL-----LHEVQLTTEVEKIKTVKESATEKLTTPVLLAKQL 49  
 Db 200 LIKEQINSLYQHLLTVIADLKNEALQLEKMKVFLRGASHELKTPLASKIL 253

RESULT 13  
 US-09-583-110-5317  
 Sequence 13, Application US/09583110  
 Patent No. 6699703  
 GENERAL INFORMATION:  
 APPLICANT: Lynn Doucette-Stamm et al.  
 TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
 TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics  
 FILE REFERENCE: PAT000-07A  
 CURRENT APPLICATION NUMBER: US/09/583, 110  
 CURRENT FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: US 09/107, 433  
 PRIOR FILING DATE: 1998-06-30  
 PRIOR APPLICATION NUMBER: US 60/085, 131  
 PRIOR FILING DATE: 1998-05-12  
 PRIOR APPLICATION NUMBER: US 60/051, 553  
 PRIOR FILING DATE: 1997-07-02  
 NUMBER OF SEQ ID NOS: 5322  
 SEQ ID NO 5317  
 LENGTH: 442  
 TYPE: PRT  
 ORGANISM: Streptococcus pneumoniae  
 US-09-583-110-5317

Query Match 24.3%; Score 61; DB 4; Length 442;  
 Best Local Similarity 33.3%; Pred. No. 23;  
 Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

QY 2 VKEPQQKYORL-----LHEVQLTTEVEKIKTVKESATEKLTTPVLLAKQL 49  
 Db 200 LIKEQINSLYQHLLTVIADLKNEALQLEKMKVFLRGASHELKTPLASKIL 253

RESULT 14  
 US-09-107-433-3720  
 Sequence 3720, Application US/09107433  
 Patent No. 6800744  
 GENERAL INFORMATION:  
 APPLICANT: Lynn A Doucette-Stamm and David Bush  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE  
 THERAPEUTICS  
 NUMBER OF SEQUENCES: 55  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02454

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: <Unknown>

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433

FILING DATE: 30-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/ 085131

FILING DATE: MAY 12, 1998

APPLICATION NUMBER: 60/085153

FILING DATE: JULY 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arinillelo, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5507

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 3720:

SEQUENCE CHARACTERISTICS:

LENGTH: 446 amino acids

TYPE: amino acid

TOPOLOGY: linear

SEQUENCE CHARACTERISTICS:

LENGTH: 644 amino acids

TYPE: amino acid

STRANDEDNESS: single

US-09-107-433-3720

RESULT 15

US-08-487-890A-6

; Sequence 6 Application US/08487890A

Patent No. 5708149

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena

APPLICANT: Harkness, Robin

APPLICANT: Schryvers, Anthony

APPLICANT: Chong, Pele

APPLICANT: Gray-Owen, Scott

APPLICANT: Yang, Yen-Ping

APPLICANT: Murdin, Andrew

APPLICANT: Klein, Michel

TITLE OF INVENTION: Lysine Receptor Genes

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney

STREET: 6th Floor, 330 University Avenue

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: MSG 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,890A

FILING DATE: 07-JUN-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/175,116

FILING DATE: 29-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/148,968

FILING DATE: 08-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 644 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-487-890A-6

Query Match 24.3%; Score 61; DB 1; Length 644;  
Best Local Similarity 33.3%; Pred. No. 23;  
Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

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DB 244 LRETDAKSQNRTKLYIOLDEADHSNRFRGKVPTKESSEEPFT 289

Search completed: November 3, 2005, 22:05:57  
Job time : 27.6952 secs

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## OM protein - protein search, using SW model

Run on: November 3, 2005, 21:53:15 ; Search time 93.712 Seconds

(without alignments)  
 232.174 Million cell updates/sec

Title: 09782816-51

Perfect score: 251

Sequence: 1 GVKETPQQKYQRLHEVQEL.....ESATEEKLTPVLLAKQLAAL 52

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters:

1867879

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:+

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 2: /cgnd\_6/podata/1/pubpaal/pct\_new\_pub.pep: \*  
 3: /cgnd\_6/podata/1/pubpaal/us06\_new\_pub.pep: \*  
 4: /cgnd\_6/podata/1/pubpaal/us06\_pubcomb.pep: \*  
 5: /cgnd\_6/podata/1/pubpaal/us07\_new\_pub.pep: \*  
 6: /cgnd\_6/podata/1/pubpaal/pcto\_pubcomb.pep: \*  
 7: /cgnd\_6/podata/1/pubpaal/us08\_new\_pub.pep: \*  
 8: /cgnd\_6/podata/1/pubpaal/us09\_pubcomb.pep: \*  
 9: /cgnd\_6/podata/1/pubpaal/us09\_pubcomb.pep: \*  
 10: /cgnd\_6/podata/1/pubpaal/us09c\_pubcomb.pep: \*  
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 15: /cgnd\_6/podata/1/pubpaal/us10c\_pubcomb.pep: \*  
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 22: /cgnd\_6/podata/1/pubpaal/us60\_pubcomb.pep: \*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB ID	Description
1	251	100.0	401	16 US-10-408-765A-1369	Sequence 1369, Appl
2	251	100.0	406	10 US-09-782-816A-53	Sequence 53, Appl
3	251	100.0	465	9 US-09-1025-298-676	Sequence 676, Appl
4	251	100.0	465	14 US-10-925-298-676	Sequence 676, Appl
5	248	98.8	183	10 US-09-782-816A-54	Sequence 54, Appl
6	248	98.8	224	16 US-10-425-115-315831	Sequence 315831, Appl
7	246	98.0	220	10 US-10-782-816A-51	Sequence 51, Appl
8	231	92.0	134	14 US-10-106-698-6730	Sequence 6730, Appl
9	113	45.0	22	10 US-09-782-816A-3	Sequence 3, Appl
10	42.6	21	10 US-09-782-816A-4	Sequence 4, Appl	
11	41.0	103	US-09-782-816A-5	Sequence 5, Appl	

## ALIGNMENTS

RESULT 1  
 US-10-408-765A-1369

Sequence 1369, Application US/10408765A

Publication No. US20040101874A1

GENERAL INFORMATION:

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Fahy, Eoin D.

APPLICANT: Zhang, Bing

APPLICANT: Gibson, Bradford W.

APPLICANT: Taylor, Steven W.

APPLICANT: Glenn, Gary M.

APPLICANT: Warnock, Dale E.

TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

FILE REFERENCE: 660088.465

CURRENT APPLICATION NUMBER: US/10/408-765A

CURRENT FILING DATE: 2003-04-04

NUMBER OF SEQ ID NOS: 3077

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 1369

LENGTH: 401

TYPE: PRT

ORGANISM: Homo sapiens

US-10-408-765A-1369

Query Match Similarity 100.0%; Score 251; DB 16; Length 401; Best Local Similarity 100.0%; Pred: No. 1: 5e-19; Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKETPQQKYQRLHEVQELTEVEKIKTIVKESATEKLTLPVLLAKQLAAL 52

Dy 94 GVKETPQQKYQRLHEVQELTEVEKIKTIVKESATEKLTLPVLLAKQLAAL 145

RESULT 2  
US-09-782-816A-53  
; Sequence 53 ; Application US/09782816A  
; Publication No. US20030032771A1  
; GENERAL INFORMATION:  
; APPLICANT: Sharp, David J.  
; APPLICANT: Scholey, Jonathon M.  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR PROLIFERATION  
; FILE REFERENCE: UC069.001A  
; CURRENT APPLICATION NUMBER: US/09/782,816A  
; CURRENT FILING DATE: 2001-02-14  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 406  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-782-816A-53

Query Match 100.0%; Score 251; DB 10; Length 406;  
Best Local Similarity 100.0%; Pred. No. 1.6e-19;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKETPQQKQRLLHEVOBLTTEVEKIKTVKESATEKLTTPVLAQAL 52  
99 GVKETPQQKQRLLHEVOBLTTEVEKIKTVKESATEKLTTPVLAQAL 150

RESULT 3  
US-09-925-298-676  
; Sequence 676 ; Application US/09925298  
; Publication No. US20020039764A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: FA103  
; CURRENT APPLICATION NUMBER: US/09/925, 298  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05881  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124, 270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 846  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 676  
; LENGTH: 465  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: SITE  
; NAME/KEY: SITE  
; LOCATION: (5)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: SITE  
LOCATION: (6)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: SITE  
LOCATION: (16)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: SITE  
LOCATION: (16)

RESULT 4  
US-09-925-298-676  
; Sequence 676 ; Application US/09925298  
; Publication No. US20020039764A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: FA103  
; CURRENT APPLICATION NUMBER: US/09/925, 298  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05881  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124, 270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 846  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 676  
; LENGTH: 465  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: SITE  
; NAME/KEY: SITE  
; LOCATION: (5)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: SITE  
LOCATION: (6)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: SITE  
LOCATION: (16)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: SITE  
LOCATION: (16)

RESULT 5  
US-09-782-816A-54  
; Sequence 54 ; Application US/09782816A  
; Publication No. US20030032771A1  
; GENERAL INFORMATION:  
; APPLICANT: Sharp, David J.  
; APPLICANT: Rogers, Gregory C.  
; APPLICANT: Scholey, Jonathon M.  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR PROLIFERATION  
; FILE REFERENCE: UC069.001A  
; CURRENT APPLICATION NUMBER: US/09/782,816A  
; CURRENT FILING DATE: 2001-02-14  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 54  
; LENGTH: 183  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-09-782-816A-54

Query Match 98.8%; Score 248; DB 10; Length 183;  
Best Local Similarity 98.1%; Pred. No. 1.3e-19;  
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKETPQQKQRLLHEVOBLTTEVEKIKTVKESATEKLTTPVLAQAL 52  
94 GVKETPQQKQRLLHEVOBLTTEVEKIKTVKESATEKLTTPVLAQAL 145  
Db 158 GVKETPQQKQRLLHEVOBLTTEVEKIKTVKESATEKLTTPVLAQAL 209

RESULT 6  
US-10-425-115-315831

RESULT 4  
US-10-102-806-676

```

; Sequence 315831, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-215322B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 315831
; LENGTH: 224
; TYPE: PRT
; ORGANISM: zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_51109C.1.pep
; US-10-425-115-315831

Query Match      98.8%; Score 248; DB 16; Length 224;
Best Local Similarity 98.1%; Pred. No. 1.7e-19; Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy   1 GVKETPQQKQYRILHEVQELTEVEKIKTVKESATEEKLTPVVLAKOAL 52
Db   47 GVKETPQQKQYRILHEVQELTEVEKIKTVKESATEEKLTPVVLAKOAL 98

RESULT 7
US-09-782-816A-51
; Sequence 51, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathon M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: UC069_001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 44
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
; OTHER INFORMATION: musculus.
; US-09-782-816A-51

Query Match      98.0%; Score 246; DB 10; Length 52;
Best Local Similarity 98.1%; Pred. No. 5e-20; Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy   1 GVKETPQQKQYRILHEVQELTEVEKIKTVKESATEEKLTPVVLAKOAL 52
Db   1 GVKETPQQKQYRILHEVQELTEVEKIKTVKESATEEKLTPVVLAKOAL 52

RESULT 8
US-10-016-698-6730
; Sequence 6730, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathon M.
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; TITLE OF INVENTION: PROLIFERATION

Query Match      92.0%; Score 231; DB 14; Length 134;
Best Local Similarity 100.0%; Pred. No. 7.1e-18; Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy   5 TPOQKQYRILHEVQELTEVEKIKTVKESATEEKLTPVVLAKOAL 52
Db   1 TPOQKQYRILHEVQELTEVEKIKTVKESATEEKLTPVVLAKOAL 48

RESULT 9
US-09-782-816A-3
; Sequence 3, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathon M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: UC069_001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
; OTHER INFORMATION: musculus.
; US-09-782-816A-3

Query Match      45.0%; Score 113; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e-05; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy   1 GVKETPQQKQYRILHEVQELTEVEKIKTVKESATEEKLTPVVLAKOAL 22
Db   1 GVKETPQQKQYRILHEVQELTEVEKIKTVKESATEEKLTPVVLAKOAL 22

RESULT 10
US-09-782-816A-4
; Sequence 4, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathon M.
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; TITLE OF INVENTION: PROLIFERATION

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; FILE REFERENCE: UC069_001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
; US-09-782-816A-4
; Query Match 42.6%; Score 107; DB 10; Length 21;
; Best Local Similarity 100.0%; Pred. No. 4.7e-05;
; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 2 VKEPQQKYQRLHLHEVQELTT 22
; Db 1 VKEPQQKYQRLHLHEVQELTT 21
; RESULT 11
; US-09-782-816A-5
; Sequence 5, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathon M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: UC069_001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
; US-09-782-816A-5
; Query Match 41.0%; Score 103; DB 10; Length 20;
; Best Local Similarity 100.0%; Pred. No. 0.00012;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 3 KETPQQKYQRLHLHEVQELTT 22
; Db 1 KETPQQKYQRLHLHEVQELTT 20
; RESULT 12
; US-09-782-816A-1
; Sequence 1, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathon M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: UC069_001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
; US-09-782-816A-4
; Query Match 42.6%; Score 107; DB 10; Length 21;
; Best Local Similarity 100.0%; Pred. No. 4.7e-05;
; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 2 VKEPQQKYQRLHLHEVQELTT 22
; Db 1 VKEPQQKYQRLHLHEVQELTT 21
; RESULT 13
; US-09-782-816A-6
; Sequence 6, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathon M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: UC069_001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
; US-09-782-816A-6
; Query Match 39.0%; Score 98; DB 10; Length 19;
; Best Local Similarity 100.0%; Pred. No. 0.00042;
; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 4 ETPOQKYQRLHLHEVQELTT 22
; Db 1 ETPOQKYQRLHLHEVQELTT 19
; RESULT 14
; US-09-782-816A-7
; Sequence 7, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathon M.
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathon M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: UC069_001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:

```

; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus  
; OTHER INFORMATION: musculus.  
US-09-782-816A-7

Query Match 37.1%; Score 93; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.0014; Mismatches 0; Indels 0; Gaps 0;  
Matches 18; Conservative 0;

Qy 5 TPQKQQLHEVQBLTT 22  
Db 1 TPQKQQLHEVQBLTT 18

RESULT 15

US-09-782-816A-8

Sequence 8, Application US/09782816A

Publication No. US20030032771A1

GENERAL INFORMATION:

APPLICANT: Sharp, David J.

APPLICANT: Rogers, Gregory C.

APPLICANT: Scholty, Jonathon M.

TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR

FILE REFERENCE: UC009.001A

CURRENT APPLICATION NUMBER: US/09-/782,816A

CURRENT FILING DATE: 2001-02-14

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 17

TYPE: PRT

ORGANISM: Unknown

FEATURE: OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus

US-09-782-816A-8

Query Match 35.1%; Score 88; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.0048; Mismatches 0; Indels 0; Gaps 0;  
Matches 17; Conservative 0;

Qy 6 PPKKQQLHEVQBLTT 22  
Db 1 PPQKQQLHEVQBLTT 17

Search completed: November 3, 2005, 22:11:40  
Job time : 93.712 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: November 3, 2005, 21:32:33 ; Search time 72.5562 Seconds  
(without alignments)  
282.516 Million cell updates/sec

Title: 09782816-52  
Perfect score: 258

Sequence: 1 GKKETPVQKCORLQIENNL.....ADEEKQSYDAVVATVISTAR 53

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext: 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_GenSeq\_16Dec04:  
1: geneseqp1980s:  
2: geneseqp1990s:  
3: geneseqp2000s:  
4: geneseqp2001s:  
5: geneseqp2002s:  
6: geneseqp2003s:  
7: geneseqp2003s:  
8: geneseqp2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	258	100.0	53	5 ABP53017	Abp53017 Cellular
2	243.5	94.4	380	4 ABP59088	Abp59088 Drosophila
3	243.5	94.4	380	5 ABP53020	Abp53020 Drosophila
4	134	44.2	22	5 ABP52991	Abp52991 Cellular
5	108	41.9	21	5 ABP52992	Abp52992 Cellular
6	105	40.7	22	5 ABP52967	Abp52967 Cellular
7	103	39.9	20	5 ABP22993	Abp52993 Cellular
8	98	38.0	19	5 ABP22994	Abp52994 Cellular
9	93	36.0	18	5 ABP52995	Abp52995 Cellular
10	88	34.1	17	5 ABP52996	Abp52996 Cellular
11	81	31.4	16	5 ABP22997	Abp52997 Cellular
12	77	29.8	15	5 ABP22998	Abp52998 Cellular
13	74	28.7	183	5 ABP53019	Abp53019 Mouse p50
14	72.5	28.1	52	5 ABP5016	Abp5016 Cellular
15	72.5	28.1	314	8 ADQ17289	Adq17289 Human s/o
16	72.5	28.1	378	6 ABP98851	Abp98851 Human s/o
17	72.5	28.1	401	7 ADJ65563	Adj65563 Human hea
18	72.5	28.1	405	18 ABP53018	Abp53018 Human p50
19	72.5	28.1	465	3 ABP5968	Abp5968 Breast can
20	72	14	5 ABP52999	Abp52999 Cellular	
21	70.5	27.9	1937	8 ADQ17242	Adq17242 Human s/o
22	70.5	27.3	1937	8 ADQ17242	Adq17242 Human s/o
23	69.5	26.9	97	4 ABP3174	Abp3174 Peptide #
24	69.5	26.9	97	4 AAM1604	Aam1604 Peptide #
25	69.5	26.9	97	4 AAM71323	Aam71323 Human s/o

#### ALIGNMENTS

RESULT 1	ABP53017	ID ABP53017 standard; peptide; 53 AA.
XX	XX	XX
AC	ABP53017;	
XX	DT	05-NOV-2002 (first entry)
XX	DE	Cellular proliferation peptide inhibitor SEQ ID NO:52.
XX	Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytial disorder; hypothalamic disorder; inflammatory; stromal disorder; macrophagal disorder; epithelial disorder; immunologic disorder.	
XX	XX	
OS	Drosophila melanogaster.	
XX	PN WO200264779-A2.	
XX	PD	22-AUG-2002.
XX	PD	21-JAN-2002; 2002W0-US001708.
XX	PR	14-FEB-2001; 2001US-00782816.
XX	(RECC ) UNIV CALIFORNIA.	
PA	PI Sharp DJ, Rogers GC, Schooley JM;	
XX	DR WPI; 2002-657599/70.	
XX	PT New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.	
XX	PS Claim 3; Page 31; 55pp; English.	
CC	The present invention describes an isolated peptide (1) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP5296 and ABP5967 and can have C-terminal and N-terminal extensions. (1) have cytosolic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such	

CC as benign or malignant tumours (renal, liver, kidney, bladder, breast,  
 CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, head and  
 CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and  
 CC neck tumours); leukaemias and lymphoid malignancies; other disorders such  
 CC as neuronal, glial, astrocytal, hypothalamic and other glandular, and  
 CC macrophagal, epithelial, stromal and blastocoelic disorders; and  
 CC inflammatory, angiogenic and immunologic disorders. The present sequence  
 CC represents a specifically claimed peptide inhibitor of cellular  
 XX proliferation from the present invention.

SQ Sequence 53 AA;

Query Match 100.0%; Score 259; DB 5; Length 53;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-26;  
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GEKETPVQKCQRLQIEMMELNNEVAALQDRKVADEEKOSYDAVATVSTAR 53  
 Db 94 GEKETPVQKCQRLQIEMMELNNEVAALQDRKVADEEKOSYDAVATVSTAR 145

RESULT 2  
 ABB59088 ABBS9088 standard; protein; 380 AA.  
 ID ABB59088  
 XX  
 AC ABB59088;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 4056.  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 OS Drosophila melanogaster.  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PR 23-MAR-2001; 2001WO-US009231.  
 XX  
 PR 23-MAR-2000; 2000US-0191637P.  
 PR 11-JUL-2000; 2000US-00614150.  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW,  
 XX  
 DR WPI; 2001-656860/75.  
 DR N-PSDB; ABL03191.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions.  
 PS Disclosure; SEQ ID NO 4056; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL0140-ABL16175) and the encoded proteins (AB55737-  
 CC ABB2072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at [ftp://ftp.wipo.int/pub/published\\_pct\\_sequences](ftp://ftp.wipo.int/pub/published_pct_sequences)  
 XX Sequence 380 AA;

SQ Sequence 53 AA;

Query Match 94.4%; Score 243.5; DB 5; Length 380;  
 Best Local Similarity 98.1%; Pred. No. 2.4e-23;  
 Matches 52; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 GEKETPVQKCQRLQIEMMELNNEVAALQDRKVADEEKOSYDAVATVSTAR 53  
 Db 94 GEKETPVQKCQRLQIEMMELNNEVAALQDRKVADEEKOSYDAVATVSTAR 145

RESULT 3  
 ABP53020 ABP53020 standard; protein; 380 AA.  
 ID ABP53020  
 XX  
 AC ABP53020;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Drosophila melanogaster p50 protein sequence SEQ ID NO:56.  
 XX  
 Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;  
 KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;  
 KW barcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;  
 KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;  
 KW glandular disorder; macrophagal disorder; epithelial disorder;  
 KW stromal disorder; blastocoelic disorder; angiogenic disorder;  
 KW immunologic disorder; p50.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200264779-A2.  
 XX  
 PD 22-AUG-2002.  
 XX  
 PI Sharp DJ, Rogers GC, Scholey JM;  
 XX  
 PR 21-JAN-2002; 2002WO-US001708.  
 PR 14-FEB-2001; 2001US-00782816.  
 XX  
 DR N-PSDB; ABQ75378.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Sharp DJ, Rogers GC, Scholey JM;  
 XX  
 PR 2002-657599/70.  
 PR  
 PT New peptide inhibitors of p50/dynamitin useful for treating cancer by  
 PT inhibiting cellular proliferation, e.g. benign or malignant tumors,  
 PT leukaemia and lymphoid malignancies, or inflammatory, angiogenic and  
 PT immunologic disorders.  
 XX  
 PS Example 1; Fig 4; 55pp; English.  
 XX  
 CC The present invention describes an isolated peptide (I) comprising or  
 CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the  
 CC sequences given in ABP296 and ABP5967 and can have C-terminal and N-  
 CC terminal extensions. (I) have cytotactic and antiinflammatory activities  
 CC and can be used as p50/dynamitin inhibitors and in gene therapy. The  
 CC peptides nucleic acid molecules and methods from the present invention  
 CC are useful for treating cancer by inhibiting cellular proliferation, such  
 CC as benign or malignant tumours (renal, liver, kidney, bladder, breast,  
 CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,  
 CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and  
 CC neck tumours); leukaemias and lymphoid malignancies, other disorders such  
 CC as neuronal, glial, astrocytal, hypothalamic and other glandular,  
 CC macrophagal, epithelial, stromal and blastocoelic disorders; and  
 CC inflammatory, angiogenic and immunologic disorders. The present sequence  
 CC represents Drosophila melanogaster p50 which is given in the  
 CC exemplification of the present invention  
 XX Sequence 380 AA;

Db 94 GEKETIPVQKCQRLQIEMNELLNEVALQVDRKVADEEKOSYDA-VATVISTAR 145.  
 RESULT 4 ABP52991 ABP52991 standard; peptide; 22 AA.  
 ID XX  
 AC XX  
 DT 05-NOV-2002 (first entry)  
 DE Cellular proliferation inhibitor related peptide SEQ ID NO:26.  
 XX  
 XX  
 KW Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;  
 KW p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma;  
 KW sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;  
 KW glial disorder; astrocytial disorder; hypothalamic disorder; inflammatory;  
 KW glandular disorder; macrophagal disorder; epithelial disorder;  
 KW stromal disorder; blastocoelic disorder; angiogenic disorder;  
 KW immunologic disorder.  
 OS Drosophila melanogaster.  
 XX  
 PN WO200264779-A2.  
 XX  
 PD 22-AUG-2002.  
 XX  
 PR 21-JAN-2002; 2002WO-US001708.  
 XX  
 PR 14-FEB-2001; 2001US-00782816.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Sharp DJ, Rogers GC, Scholey JM;  
 DR WPI; 2002-657599/70.  
 XX  
 PT New peptide inhibitors of p50/dynamitin useful for treating cancer by  
 PT inhibiting cellular proliferation, e.g. benign or malignant tumors;  
 PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and  
 PT immunologic disorders.  
 PS Claim 1; Page 30; 55pp; English.  
 XX  
 CC The present invention describes an isolated peptide (I) comprising or  
 having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the  
 sequences given in ABP52966 and ABP52967 and can have C-terminal and N-  
 terminal extensions. (I) have cyrostatic and antiinflammatory activities  
 and can be used as p50/dynamitin inhibitors and methods from the present invention  
 are useful for treating cancer by inhibiting cellular proliferation, such  
 as benign or malignant tumors (renal, liver, kidney, bladder, breast,  
 CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva,  
 CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and  
 CC neck tumours); leukaemias and lymphoid malignancies, other disorders such  
 CC as neuronal, glial, astrocytial, hypothalamic and other glandular,  
 CC macrophagal, epithelial, stromal and blastocoelic disorders; and  
 CC inflammatory, angiogenic and immunologic disorders. The present sequence  
 CC represents a peptide that can be N-terminally added to (P2)  
 SQ Sequence 22 AA;  
 Query Match 44.2%; Score 114; DB 5; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 8e-08; Indels 0; Gaps 0;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 EKETIPVQKCQRLQIEMNELLIN 22  
 Db 1 GEKETIPVQKCQRLQIEMNELLIN 22  
 RESULT 6 ABP52967  
 ID ABP52967 Standard; peptide; 22 AA.  
 XX  
 AC ABP52967;

				DT	05-NOV-2002 (First entry)
XX	DE	cellular proliferation inhibitor related peptide SEQ ID NO:2.		KW	sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;
KW	Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;		KW	glial disorder; astrocytial disorder; hypothalamic disorder; inflammatory;	
KW	p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;		KW	glandular disorder; macrophagal disorder; epithelial disorder;	
KW	sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;		KW	stromal disorder; blastocoelic disorder; angiogenic disorder;	
KW	glial disorder; astrocytial disorder; hypothalamic disorder; inflammatory;		KW	immunologic disorder.	
KW	glandular disorder; macrophagal disorder; epithelial disorder;		OS	Drosophila melanogaster.	
KW	stromal disorder; blastocoelic disorder; angiogenic disorder;		XX		
KW	immunologic disorder.		XX		
OS	Drosophila melanogaster.		XX		
XX	W0200264779-A2.		PN		
XX	PR		XX		
PD	22-AUG-2002.		PA		
XX	21-JAN-2002; 2002WO-US001708.		XX		
PF	14-FEB-2001; 2001US-00782816.		PI		
XX	(REGC ) UNIV CALIFORNIA.		Sharp DJ, Rogers GC, Scholey JM;		
PA			XX		
PI	Sharp DJ, Rogers GC, Scholey JM;		DR		
XX	WPI; 2002-657599/70.		XX		
PT	New peptide inhibitors of p50/dynamitin useful for treating cancer by		PR		
PT	inhibiting cellular proliferation, e.g. benign or malignant tumors		XX		
PT	leukemia and lymphoid malignancies, or inflammatory, angiogenic and		PA		
PT	immunologic disorders.		XX		
XX	Claim 1; Page 29; 55pp; English.		PI		
PS	The present invention describes an isolated peptide (I) comprising or		XX		
CC	having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the		DR		
CC	sequences given in ABP2966 and ABP2967 and can have C-terminal and N-		XX		
CC	terminal extensions, (I) have cytostatic and antiinflammatory activities		PR		
CC	and can be used as p50/dynamitin inhibitors and in gene therapy. The		XX		
CC	peptides, nucleic acid molecules and methods from the present invention		PA		
CC	are useful for treating cancer by inhibiting cellular proliferation, such		XX		
CC	as benign or malignant tumours (renal, liver, kidney, bladder, breast,		PI		
CC	gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid,		XX		
CC	hepatic carcinomas, sarcomas, glioblastomas, and various head and		PR		
CC	neck tumours); leukaemias and lymphoid malignancies, other disorders such		XX		
CC	as neuronal, glial, astrocytal, hypothalamic and other glandular,		PA		
CC	macrophagal, epithelial, stromal and blastocoelic disorders; and		XX		
CC	inflammatory, angiogenic and immunologic disorders. The present sequence		PI		
CC	represents a peptide that can be N-terminally added to (P2).		XX		
SQ	Sequence 22 AA;		SQ		
Query Match	40.7%; Score 105; DB 5; Length 22;		Query Match	39.9%; Score 103; DB 5; Length 20;	
QY	Best Local Similarity 100.0%; Pred. No. 1 2e-05; Mismatches 0; Indels 0; Gaps 0;		QY	Best Local Similarity 100.0%; Pred. No. 2e-06; Mismatches 0; Indels 0; Gaps 0;	
Db	Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Db	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
RESULT 7			RESULT 8		
ABP2993			ABP2994		
ID	ABP2993 standard; peptide; 20 AA.		ID	ABP2994 standard; peptide; 19 AA.	
XX			XX		
AC	ABP2993;		AC	ABP2994;	
XX			XX		
DT	05-NOV-2002 (first entry)		DT		
XX	Cellular proliferation inhibitor related peptide SEQ ID NO:29.		XX		
XX	Cellular proliferation inhibitor related peptide SEQ ID NO:29.		DE		
XX	Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;		XX		
XX	p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;		KW		
XX	barcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;		KW		
XX	glial disorder; astrocytial disorder; hypothalamic disorder; inflammatory;		KW		
XX	glandular disorder; macrophagal disorder; epithelial disorder;		KW		
XX	stromal disorder; blastocoelic disorder; angiogenic disorder;		KW		
KW	immunologic disorder.		KW		

XX  
OS Drosophila melanogaster.  
XX  
PN WO200264779-A2.  
XX  
PD 22-AUG-2002.  
XX  
PR 21-JAN-2002; 2002WO-US001708.  
XX  
PR 14-FEB-2001; 2001US-00782816.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
PT Sharp DJ, Rogers GC, Scholey JM;  
PT  
XX DR WPI; 2002-657599/70.  
XX  
PT New peptide inhibitors of p50/dynamitin useful for treating cancer by  
PT inhibiting cellular proliferation, e.g. benign or malignant tumors,  
PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and  
PT immunologic disorders.  
XX  
PS Claim 1; Page 30; 55pp; English.  
XX  
CC The present invention describes an isolated peptide (I) comprising or  
CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the  
CC sequences given in ABP5296 and ABP5297 and can have C-terminal and N-  
CC terminal extensions. (I) have cytostatic and anti-inflammatory activities  
CC and can be used as p50/dynamitin inhibitor and in gene therapy. The  
CC peptides, nucleic acid molecules and methods from the present invention  
CC are useful for treating cancer by inhibiting cellular proliferation, such  
CC as benign or malignant tumours (renal, liver, kidney, bladder, breast,  
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva,  
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and  
CC neck tumours); leukaemias and lymphoid malignancies, other disorders such  
CC as neuronal, glial, astrocytic, hypothalamic and other glandular,  
CC macrophagal, epithelial, stromal and blastocoeleic disorders; and  
CC inflammatory, angiogenic and immunologic disorders. The present sequence  
CC represents a peptide that can be N-terminally added to (P2)  
SQ Sequence 19 AA;

Qy	4 ETPVQKQRQIQLQEMNLIN 22	38.0%; Score 98; DB 5; Length 19;
DB	1 ETPVQKQRQIQLQEMNLIN 19	Best Local Similarity 100.0%; Pred. No. 8.6e-06; Mismatches 0; Indels 0; Gaps 0;

RESULT 9

ID ABP5295  
XX ABP5295 standard; Peptide; 18 AA.

AC ABP5295;  
DT 05-NOV-2002 (first entry)

DB Cellular proliferation inhibitor related peptide SEQ ID NO:30.

XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;  
KW p50 inhibitor; dynamin inhibitor; gene therapy; tumour; carcinoma;  
KW sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;  
KW glial disorder; astrocytoma; hypothalamic disorder; inflammatory;  
KW glandular disorder; macrophagal disorder; epithelial disorder; inflammatory;  
KW stromal disorder; blastocoeleic disorder; angiogenic disorder;  
KW immunologic disorder.

OS Drosophila melanogaster.

XX WO200264779-A2.

XX 22-AUG-2002.

XX PR 21-JAN-2002; 2002WO-US001708.

XX PA (REGC ) UNIV CALIFORNIA.  
PT Sharp DJ, Rogers GC, Scholey JM;  
PT  
XX DR WPI; 2002-657599/70.  
XX  
PT New peptide inhibitors of p50/dynamitin useful for treating cancer by  
PT inhibiting cellular proliferation, e.g. benign or malignant tumors,  
PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and  
PT immunologic disorders.  
XX  
PS Claim 1; Page 30; 55pp; English.  
XX  
CC The present invention describes an isolated peptide (I) comprising or  
CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the  
CC sequences given in ABP5296 and ABP5297 and can have C-terminal and N-  
CC terminal extensions. (I) have cytostatic and anti-inflammatory activities  
CC and can be used as p50/dynamitin inhibitors and in gene therapy. The  
CC peptides, nucleic acid molecules and methods from the present invention  
CC are useful for treating cancer by inhibiting cellular proliferation, such  
CC as benign or malignant tumours (renal, liver, kidney, bladder, breast,  
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva,  
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and  
CC neck tumours); leukaemias and lymphoid malignancies, other disorders such  
CC as neuronal, glial, astrocytic, hypothalamic and other glandular,  
CC macrophagal, epithelial, stromal and blastocoeleic disorders; and  
CC inflammatory, angiogenic and immunologic disorders. The present sequence  
CC represents a peptide that can be N-terminally added to (P2)  
SQ Sequence 18 AA;

Qy	5 TPVQKQRQIQLQEMNLIN 22	Query Match 36.0%; Score 93; DB 5; Length 18;
DB	1 TPVQKQRQIQLQEMNLIN 18	Best Local Similarity 100.0%; Pred. No. 3.7e-05; Mismatches 0; Indels 0; Gaps 0;

RESULT 10

ID ABP5296  
XX ABP5296 standard; peptide; 17 AA.

AC ABP5296;  
DT 05-NOV-2002 (first entry)

XX Cellular proliferation inhibitor related peptide SEQ ID NO:31.

KW Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;  
KW p50 inhibitor; dynamin inhibitor; gene therapy; tumour; carcinoma;  
KW sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;  
KW glial disorder; astrocytoma; hypothalamic disorder; inflammatory;  
KW glandular disorder; macrophagal disorder; epithelial disorder; inflammatory;  
KW stromal disorder; blastocoeleic disorder; angiogenic disorder;  
KW immunologic disorder.

OS Drosophila melanogaster.

XX WO200264779-A2.

XX 22-AUG-2002.

XX PR 21-JAN-2002; 2002WO-US001708.

XX PA (REGC ) UNIV CALIFORNIA.  
PT Sharp DJ, Rogers GC, Scholey JM;  
PT  
XX DR WPI; 2002-657599/70.  
XX  
PT New peptide inhibitors of p50/dynamitin useful for treating cancer by  
PT inhibiting cellular proliferation, e.g. benign or malignant tumors,  
PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and  
PT immunologic disorders.  
XX  
PS Claim 1; Page 30; 55pp; English.  
XX  
CC The present invention describes an isolated peptide (I) comprising or  
CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the  
CC sequences given in ABP5296 and ABP5297 and can have C-terminal and N-  
CC terminal extensions. (I) have cytostatic and anti-inflammatory activities  
CC and can be used as p50/dynamitin inhibitors and in gene therapy. The  
CC peptides, nucleic acid molecules and methods from the present invention  
CC are useful for treating cancer by inhibiting cellular proliferation, such  
CC as benign or malignant tumours (renal, liver, kidney, bladder, breast,  
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva,  
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and  
CC neck tumours); leukaemias and lymphoid malignancies, other disorders such  
CC as neuronal, glial, astrocytic, hypothalamic and other glandular,  
CC macrophagal, epithelial, stromal and blastocoeleic disorders; and  
CC inflammatory, angiogenic and immunologic disorders. The present sequence  
CC represents a peptide that can be N-terminally added to (P2)  
SQ Sequence 18 AA;

Qy	5 TPVQKQRQIQLQEMNLIN 22	Query Match 36.0%; Score 93; DB 5; Length 18;
DB	1 TPVQKQRQIQLQEMNLIN 18	Best Local Similarity 100.0%; Pred. No. 3.7e-05; Mismatches 0; Indels 0; Gaps 0;



PT immunologic disorders.

XX Claim 1; Page 30; 55pp; English.

CC The present invention describes an isolated peptide (I) comprising or  
 CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the  
 CC sequences given in ABP2966 and ABP5267 and can have C-terminal and N-  
 CC terminal extensions. (I) have cytostatic and antiinflammatory activities  
 CC and can be used as p50/dynamitin inhibitors and in gene therapy. The  
 CC peptides, nucleic acid molecules and methods from the present invention  
 CC are useful for treating cancer by inhibiting cellular proliferation, such  
 CC as benign or malignant tumours (renal, liver, kidney, bladder, breast,  
 CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,  
 CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and  
 CC neck tumours); leukaemias and lymphoid malignancies, other disorders such  
 CC as neuronal, glial, astrocytal, hypothalamic and other glandular,  
 CC macrophagal, epithelial, stromal and blastocoelic disorders; and  
 CC represents a peptide that can be N-terminally added to (P2).

SQ Sequence 15 AA;

Query Match 29.8%; Score 77; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.0038; Mismatches 0; Indels 0; Gaps 0;

QY 8 QKCQRLQIEMMELIN 22  
 DB 1 QKCQRLQIEMMELIN 15

RESULT 13

ABP53019 ABP53019 standard; protein; 183 AA.

AC ABB53019;  
 XX DT 05-NOV-2002 (first entry)  
 DE Mouse p50 amino acid sequence SEQ ID NO:54.

XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;  
 KW p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma;  
 KW sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;  
 KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;  
 KW stromal disorder; macrophagal disorder; epithelial disorder;  
 KW immunologic disorder. OS Mus musculus.  
 KW immunologic disorder. OS Synthetic.

OS Mus musculus.

XX WO200264779-A2.

XX PD 22-AUG-2002.  
 XX PR 21-JAN-2002; 2002WO-US001708.  
 XX PR 14-FEB-2001; 2001US-00782816.  
 XX PA (REGC ) UNIV CALIFORNIA.  
 XX DR WPI; 2002-657599/70.

PT New peptide inhibitors of p50/dynamitin useful for treating cancer by

PT inhibiting cellular proliferation, e.g. benign or malignant tumors,  
 PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and  
 PT immunologic disorders.

XX Disclosure; Fig 2; 55pp; English.

RESULT 14

ABP53016 ABP53016 standard; peptide; 52 AA.

AC ABP53016;  
 XX DT 05-NOV-2002 (first entry)

DE Cellular proliferation peptide inhibitor SEQ ID NO:51.  
 KW Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;  
 KW p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma;  
 KW sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;  
 KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;  
 KW stromal disorder; macrophagal disorder; epithelial disorder;  
 KW immunologic disorder.

XX Homo sapiens.

OS Mus musculus.

OS Synthetic.

OS

FH Key location/Qualifiers  
 FT Misc-difference 44 /label= Leu, Val  
 FT /notes "Leu in humans and Val in Mus musculus"

XX PN WO200264779-A2.  
 XX PD 22-AUG-2002.  
 XX PR 21-JAN-2002; 2002WO-US001708.  
 XX PA 14-FEB-2001; 2001US-00782816.  
 XX PR (REGC ) UNIV CALIFORNIA.  
 XX PI Sharp DJ, Rogers GC, Scholey JM;  
 XX DR WPI; 2002-657599/70.

PT New peptide inhibitors of p50/dynamitin useful for treating cancer by  
 PT inhibiting cellular proliferation, e.g. benign or malignant tumors,  
 PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and  
 PT immunologic disorders.

XX Disclosure; Fig 2; 55pp; English.

The present invention describes an isolated peptide (I) comprising or

CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the  
 CC sequences given in ABP2966 and ABP5267 and can have C-terminal and N-  
 CC terminal extensions. (I) have cytostatic and antiinflammatory activities  
 CC and can be used as p50/dynamitin inhibitors and in gene therapy. The  
 CC peptides, nucleic acid molecules and methods from the present invention  
 CC are useful for treating cancer by inhibiting cellular proliferation, such  
 CC as benign or malignant tumours (renal, liver, kidney, bladder, breast,  
 CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,  
 CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and  
 CC neck tumours); leukaemias and lymphoid malignancies, other disorders such  
 CC as neuronal, glial, astrocytal, hypothalamic and other glandular,  
 CC macrophagal, epithelial, stromal and blastocoelic disorders; and  
 CC inflammatory, angiogenic and immunologic disorders. The present sequence  
 CC represents mouse p50 which is given in the exemplification of the present  
 CC invention

SQ Sequence 183 AA;

Query Match 28.7%; Score 74; DB 5; Length 183;

Best Local Similarity 35.8%; Pred. No. 0.23; Mismatches 24; Indels 0; Gaps 0;

QY 1 GEKEPVPKCQRLQIEMMELINNEALQVDRKVADEEKSYDAVATVISTAR 53  
 DB 94 GVKEPVPQKQVORLHLHEVQBLTTEVEKIKTVKESATEKLTUPVVLAKOLAALK 146

PS Claim 2; Page 31; 55pp; English.

XX  
CC The present invention describes an isolated peptide (I) comprising or  
CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the  
CC sequences given in ABP2966 and ABP52967 and can have C-terminal and N-  
CC terminal extensions. (I) have cyrostatic and anti-inflammatory activities  
CC and can be used as p50/dynamitin inhibitors and in gene therapy. The  
CC peptides, nucleic acid molecules and methods from the present invention  
CC are useful for treating cancer by inhibiting cellular proliferation, such  
CC as benign or malignant tumours (renal, liver, kidney, bladder, breast,  
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva,  
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and  
CC neck tumours); leukemias and lymphoid malignancies, other disorders such  
CC as neuronal, glial, astrocytic, hypothalamic and other glandular,  
CC macrophagal, epithelial, stromal and blastococel disorders; and  
CC inflammatory, angiogenic and immunologic disorders. The present sequence  
CC represents a specifically claimed peptide inhibitor of cellular  
CC proliferation from the present invention

XX sequence 52 AA;

Query Match 28.1%; Score 72.5; DB 5; Length 52;

Best Local Similarity 48.7%; Pred. No. 0.072; 19; Mismatches 5; Indels 1; Gaps 1;

QY 1 GEKETPVOKCQLQTEMNELLNEVALQVD-RKVADBEK 38  
Db ||||| : ||| :: ||| : ||| : |||

1 GVKETPQKYQRLHLHEVOELTTEVKITVKESATEK 39

RESULT 15

ABM81421 standard; protein; 314 AA.

ID ABM81421; AC ABM81421;

XX DT 18-NOV-2004 (first entry)

DE Tumour-associated antigenic target (TAT) polypeptide PRO82191, SEQ:3675.  
XX  
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;  
KW tumour; diagnosis; cell proliferative disorder; breast cancer;  
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;  
KW central nervous system cancer; bladder cancer; pancreatic cancer;  
KW chromosome identification; melanoma; leukaemia; hybridisation probe;  
KW gene therapy; cytostatic.

OS Homo sapiens.  
XX  
PN WO2004030615-A2.  
XX  
PD 15-APR-2004.  
XX  
PF 29-SEP-2003; 2003W0-US028547.  
XX  
PR 02-OCT-2002; 2002US-0414971P.  
XX  
PA (GEITH ) GENENTECH INC.  
XX  
PI Wu TD, Zhang Z, Zhou Y;  
XX  
DR WPI; 2004-347921/32.  
DR N-P5DB; ACN39497.

XX  
PT New tumor-associated antigenic target polypeptides and nucleic acids,  
PT useful in preparing a medicament for treating or detecting a  
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or  
PT prostate cancer or tumor.

XX  
PS Claim 12; SEQ ID NO 3675; 7273pp; English.

XX The invention relates to human tumour-associated antigenic target (TAT)

CC polypeptides, and their related nucleic acids. The TAT polypeptides are  
CC overexpressed in cancer tissues compared to normal tissues, and may thus  
CC serve as effective targets for the diagnosis and treatment of cancer in  
mammals. The invention also relates to nucleic acid and polypeptide  
CC sequences at least 80% identical to the TAT nucleic acids and  
CC polypeptides; expression vectors and host cells comprising a TAT nucleic  
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic  
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a  
CC TAT polypeptide; and methods and compositions for the treatment or  
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,  
CC antibodies, antagonists, binding molecules and compositions are useful  
CC for diagnosing or treating a cell proliferative disorder associated with  
CC increased TAT expression, particularly cancer such as breast cancer,  
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder  
CC cancer, pancreatic cancer, cervical cancer, cancers of the central  
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be  
CC used as hybridization probes, in chromosome and gene mapping, in  
CC chromosome identification and in gene therapy. The present sequence  
CC represents a TAT polypeptide of the invention

XX Sequence 314 AA;

Query Match 28.1%; Score 72.5; DB 8;

Best Local Similarity 48.7%; Pred. No. 0.71; 19; Mismatches 5; Indels 1; Gaps 1;

QY 1 GEKETPVOKCQLQTEMNELLNEVALQVD-RKVADBEK 38  
Db ||||| : ||| :: ||| : ||| : |||

7 GVKETPQKYQRLHLHEVOELTTEVKITVKESATEK 45

Search completed: November 3, 2005, 21:57:31  
Job time : 73.5562 secs

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## OM protein - protein search, using bw model

Run on: November 3, 2005, 21:43:09 ; Search time 19.2727 Seconds  
(without alignments)

Title: 09782816-52  
Perfect score: 258  
Sequence: 1 GEKETIVQKCORLQIEMNEL.....ADEEKOSYDAWATVISTAR 53

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext: 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pix1:\*\*  
2: pix2:\*\*  
3: pix3:\*\*  
4: pix4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	70.5	27.3	I38055	myosin heavy chain, perinatal skeletal muscle - human
2	69.5	26.9	AC1523	hypothetical prote
3	68	26.4	H72670	hypothetical prote
4	67	26.2	HT0314	hypothetical prote
5	66	25.6	508	hypothetical prote
6	65	25.2	T38345	hypothetical prote
7	64.5	25.0	157	hypothetical prote
8	63.5	24.6	676	hypothetical prote
9	63.5	24.6	698	hypothetical prote
10	63.5	24.6	1938	hypothetical prote
11	63	24.6	111	hypothetical prote
12	62.5	24.2	222	hypothetical prote
13	62.5	24.2	955	hypothetical prote
14	62.5	24.2	1938	hypothetical prote
15	62	24.0	2	hypothetical prote
16	62	24.0	230	hypothetical prote
17	62	24.0	1938	hypothetical prote
18	62	24.0	743	hypothetical prote
19	62	24.0	1133	hypothetical prote
20	60.5	23.4	900	hypothetical prote
21	60	23.3	1050	hypothetical prote
22	59.5	23.3	2	hypothetical prote
23	59.5	23.1	534	hypothetical prote
24	59	23.1	240	hypothetical prote
25	59.5	23.1	936	hypothetical prote
26	59	22.9	1940	hypothetical prote
27	59	22.9	214	hypothetical prote
28	58.5	22.7	503	hypothetical prote
29	58.5	22.7	222	hypothetical prote

Score	Length	DB ID	Score	Length	DB ID
30	22.5	P00514	58	22.5	hemagglutinin HR2
31	58	S07537	58	22.5	myosin heavy chain
32	58	G97884	22.5	argininosuccinate	
33	58	621	2	myosin heavy chain	
34	58	T00617	22.5	endoatyle-specific	
35	58	866	2	paramyosin - caeno	
36	58	872	2	hypothetical prote	
37	58	1255	2	diaphanous protein	
38	58	22.5	2297	hypothetical prote	
39	57.5	22.3	271	33K cytoskeletal p	
40	57.5	22.3	1	giardin beta chain	
41	57.5	22.3	410	hypothetical prote	
42	57.5	22.3	560	protein YKR029c ho	
43	57.5	22.3	553382	hypothetical prote	
44	57.5	22.3	629	hypothetical prote	
45	57.5	22.3	2	myosin heavy chain	
46	57.5	22.3	791	hypothetical prote	
47	57.5	22.3	2	myosin heavy chain	
48	57.5	22.3	876	hypothetical prote	
49	57.5	22.3	2	myosin heavy chain	

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

283416

Maximum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pix1:\*\*  
2: pix2:\*\*  
3: pix3:\*\*  
4: pix4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	70.5	27.3	I38055	myosin heavy chain, perinatal skeletal muscle - human
2	69.5	26.9	AC1523	hypothetical prote
3	68	26.4	H72670	hypothetical prote
4	67	26.2	HT0314	hypothetical prote
5	66	25.6	508	hypothetical prote
6	65	25.2	T38345	hypothetical prote
7	64.5	25.0	157	hypothetical prote
8	63.5	24.6	676	hypothetical prote
9	63.5	24.6	698	hypothetical prote
10	63.5	24.6	1938	hypothetical prote
11	63	24.6	111	hypothetical prote
12	62.5	24.2	222	hypothetical prote
13	62.5	24.2	955	hypothetical prote
14	62.5	24.2	1938	hypothetical prote
15	62	24.0	2	hypothetical prote
16	62	24.0	230	hypothetical prote
17	62	24.0	1938	hypothetical prote
18	62	24.0	743	hypothetical prote
19	62	24.0	1133	hypothetical prote
20	60.5	23.4	900	hypothetical prote
21	60	23.3	1050	hypothetical prote
22	59.5	23.3	2	hypothetical prote
23	59.5	23.1	534	hypothetical prote
24	59	23.1	240	hypothetical prote
25	59.5	23.1	936	hypothetical prote
26	59	22.9	1940	hypothetical prote
27	59	22.9	214	hypothetical prote
28	58.5	22.7	503	hypothetical prote
29	58.5	22.7	222	hypothetical prote

Score	Length	DB ID	Score	Length	DB ID
30	22.5	P00514	58	22.5	hemagglutinin HR2
31	58	S07537	58	22.5	myosin heavy chain
32	58	G97884	22.5	argininosuccinate	
33	58	621	2	myosin heavy chain	
34	58	T00617	22.5	endoatyle-specific	
35	58	866	2	paramyosin - caeno	
36	58	872	2	hypothetical prote	
37	58	1255	2	diaphanous protein	
38	58	22.5	2297	hypothetical prote	
39	57.5	22.3	271	33K cytoskeletal p	
40	57.5	22.3	1	giardin beta chain	
41	57.5	22.3	410	hypothetical prote	
42	57.5	22.3	560	protein YKR029c ho	
43	57.5	22.3	553382	hypothetical prote	
44	57.5	22.3	629	hypothetical prote	
45	57.5	22.3	2	myosin heavy chain	
46	57.5	22.3	791	hypothetical prote	
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49	57.5	22.3	2	myosin heavy chain	

Score	Length	DB ID	Score	Length	DB ID
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31	58	S07537	58	22.5	myosin heavy chain
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33	58	621	2	myosin heavy chain	
34	58	T00617	22.5	endoatyle-specific	
35	58	866	2	paramyosin - caeno	
36	58	872	2	hypothetical prote	
37	58	1255	2	diaphanous protein	
38	58	22.5	2297	hypothetical prote	
39	57.5	22.3	271	33K cytoskeletal p	
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42	57.5	22.3	560	protein YKR029c ho	
43	57.5	22.3	553382	hypothetical prote	
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49	57.5	22.3	2	myosin heavy chain	

Score	Length	DB ID	Score	Length	DB ID
30	22.5	P00514	58	22.5	hemagglutinin HR2
31	58	S07537	58	22.5	myosin heavy chain
32	58	G97884	22.5	argininosuccinate	
33	58	621	2	myosin heavy chain	
34	58	T00617	22.5	endoatyle-specific	
35	58	866	2	paramyosin - caeno	
36	58	872	2	hypothetical prote	
37	58	1255	2	diaphanous protein	
38	58	22.5	2297	hypothetical prote	
39	57.5	22.3	271	33K cytoskeletal p	
40	57.5	22.3	1	giardin beta chain	
41	57.5	22.3	410	hypothetical prote	
42	57.5	22.3	560	protein YKR029c ho	
43	57.5	22.3	553382	hypothetical prote	
44	57.5	22.3	629	hypothetical prote	
45	57.5	22.3	2	myosin heavy chain	
46	57.5	22.3	791	hypothetical prote	
47	57.5	22.3	2	myosin heavy chain	
48	57.5	22.3	876	hypothetical prote	
49	57.5	22.3	2	myosin heavy chain	

A;Experimental source: strain K1  
A;Gene: APE0790  
C;Generic:  
Query Match 26.4%; Score 68; DB 2; Length 297;  
Best Local Similarity 46.7%; Pred. No. 3.1;  
Matches 14; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
QY 12 RLQTEMNELLNEVAALQVDRKVADEEKQSY 41  
|||: |||: |||: |||: |||: |||:  
29 RLUKEKKELINEVALRBERRKASREKREY 58

**RESULT 4**

H70314 hypothetical protein aq\_157 - Aquifex aeolicus  
C;Species: Aquifex aeolicus  
C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C;Accession: H70314  
R;Beckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,  
V.  
Nature 392, 353-358, 1998  
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus  
A;Reference number: A703000; MUID:98196666; PMID:9537320  
A;Accession: H70314  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-162 <AOF>  
A;Cross-references: UNIPROT:O66547; GB:AB000676; NID:g2982884; PIDN:AC06512.1;  
A;Experimental source: strain VF5  
C;Genetics:

A;Gene: aq\_157

hypothetical protein SPAC24C9.05c - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1993 #sequence\_revision 03-Dec-1993 #text\_change 09-Jul-2004

C;Accession: T8346

R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, August 1995

A;Reference number: 221787

A;Accession: T8346

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-730 <MUR>

A;Cross-references: UNIPROT:OJ3965; EMBL:Z98601; PIDN:CAB11262.1; GSDB:GN00066; SPDB:SPAC24C9.05c

A;Genes: SPBP:SPAC24C9.05c

A;Map position: 1

RESULT 7

B81688 Query Match 25.3%; Score 65; DB 2; Length 730;保守性氨基酸比对结果

Best Local Similarity 28.2%; Pred. No. 17; Matches 20; Mismatches 11; Indels 20; Gaps 2;保守性氨基酸比对结果

C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C;Accession: B81688

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.; Nucleic Acids Res., 28, 1197-1206, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; PMID:20150255; PMID:1684935

A;Accession: B81688

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-157 <NET>

A;Cross-references: UNIPROT:Q2PK98; GB:AB002325; GB:AE002160; NID:g7190604; PIDN:AAF3940

A;Experimental source: strain Nigg (MoPn)

A;Gene: TCC0569

A;Genetics:

Query Match 25.0%; Score 64.5; DB 2; Length 157;保守性氨基酸比对结果

Best Local Similarity 31.5%; Pred. No. 3.9; Matches 17; Conservative 12; Mismatches 22; Indels 3; Gaps 2;保守性氨基酸比对结果

QY 2 EKETPPVOKCQLQIENMLNEVAALQVDRKVADEEKQSIDAV-WATVISTAR 53

Db 24 EKIAPVSDCKKLEAELKFKEVAVAK-DRYLQRWENVRSLPQWHAIKKR 76

RESULT 8

S00084 myosin heavy chain, fast skeletal muscle - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004

C;Accession: S00084; SI4807

R;Maeda, K.; Sczakiel, G.; Wittlinghofer, A.

Eur. J. Biochem. 167, 97-102, 1987

A;Title: Characterization of cDNA coding for the complete light meromyosin portion of a

A;Accession: S00084

A;Reference number: S00084; MUID:87304245; PMID:3305014

A;Molecule type: mRNA

A;Residues: 1-676 <MAB>

A;CROSS-References: UNIK01; P02567; EMBL:X05958; NCBI:J051622; PDB:CAAB4391.1; PDB:9139424  
A;Note: the sequence from FIG. 5 is inconsistent with that from FIG. 3 in having 561-Arg  
R;Meda, K.; Roehl, A.; Maeda, Y.; Kalbitzer, H.R.; Wittinghofer, A.  
FEBs Lett., 281, 23-26, 1991

A;Title: Rabbit skeletal muscle myosin. Unfolded carboxyl-terminus and its role in molecular  
A;Reference number: S14807; MNUID:91200294; PMID:2015900  
A;PDB ID: 21-676/Domain: light meromyosin <LM2>  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 668-676 <MA2>  
C;Superfamily: myosin heavy chain; myosin motor domain homology  
C;Keywords: actin binding; AMP; coiled coil; muscle; skeletal muscle  
P;21-676/Domain: light meromyosin <LM2>

RESULT 9  
55296 myosin heavy chain - rainbow trout (fragment)  
C;Species: Oncorhynchus mykiss (rainbow trout)  
C;Date: 19-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C;Accession: S52696  
R;Gauvry, L.L.; Faconneau, B.B.  
submitted to the EMBL Data Library, March 1995  
A;Description: Cloning of a fast skeletal myosin heavy chain expressed both in embryo and adult.  
A;Reference number: S52696  
A;Accession: S52696  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-698 <GAU>  
A;Cross-references: UNIPROT:Q91208; EMBL:248794; NID:975570; PTDN:CAA88724.1; PID:97557  
C;Superfamily: myosin heavy chain; myosin motor domain homology  
C;Keywords: ATP

Query Match 24.6%; Score 63.5; DB 2; Length 676;  
Best Local Similarity 35.1%; Pred. No. 24;  
Matches 20; Conservative 13; Mismatches 13; Indels 11; Gaps 3;  
C;Status: preliminary

QY 1 GEKETPVOKQRLQEMNLNEVALQDRKVA--DEE---KOSYDAVATVIST 51  
Db 312 GTLHEBESKLIRVQELNGKE----VDRKIAKDEEMQIKENSQRVDMSMQST 363

RESULT 10  
JX0178 myosin heavy chain, fast skeletal muscle, adult [validated] - chicken  
N;Contains: myosin ATPase (EC 3.6.4.1)  
C;Species: Gallus gallus (chicken)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C;Accession: PX0050; PX0051; PX0052; JX0178; A26365; S02082; PW0009; S39081; S24351; S05  
R;Hayashida, M.; Maita, T.; Matsuda, G.  
J. Biocell. 110, 54-59, 1991  
A;Title: The primary structure of skeletal muscle myosin heavy chain: I. Sequence of the  
A;Reference number: PX0050; MNUID:92041767; PMID:1939027  
A;Accession: PX0050  
A;Molecule type: protein  
A;Residues: 1-205 <HAY>  
A;Cross-references: UNIPROT:Q90913; UNIPROT:Q90909  
J; Biocell. 110, 60-67, 1991  
R;Komine, Y.; Maita, T.; Matsuda, G.  
A;Title: The primary structure of skeletal muscle myosin heavy chain: II. Sequence of the  
A;Reference number: PX0051; MNUID:92041768; PMID:1939028  
A;Accession: PX0051  
A;Molecule type: protein  
A;Residues: 206-636 <KOM>  
R;Maita, T.; Miyashita, T.; Matsuzono, K.; Tanioka, Y.; Matsuda, G.

J. Biochem. 110, 68-74, 1991  
 A;Title: The primary structure of skeletal muscle myosin heavy chain: III. Sequence of the  
 A;Reference number: PX0052; MUID:92041769; PMID:1939029  
 A;Accession: PX0052  
 A;Molecule type: protein  
 A;Residues: T, Yajima, E.; Nagata, S.; Miyanishi, T.; Nakayama, S.; Matsuda, G.  
 R;Maita, T.; Yajima, E.; Nagata, S.; Miyanishi, T.; Nakayama, S.; Matsuda, G.  
 J. Biochem. 110, 75-87, 1991  
 A;Title: The primary structure of skeletal muscle myosin heavy chain: IV. Sequence of the  
 A;Reference number: JX0178; MUID:92041770; PMID:1939030  
 A;Accession: JX0178  
 A;Molecule type: protein  
 A;Residues: 833-1938 <WA2>  
 R;Maita, T.; Hayashida, M.; Tanioka, Y.; Komine, Y.; Matsuda, G.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 416-420, 1987  
 A;Title: The primary structure of the myosin head.  
 A;Reference number: A26365; MUID:87092420; PMID:3467365  
 A;Accession: A26365  
 A;Molecule type: protein  
 A;Residues: I-129, X, 131-139, 141-550, X, 552-754, X, 756-784, QL, 787-804, 806-810 <MA3>  
 R;Watanabe, B.  
 Biol. Chem. Hoppe-Seyler 370, 55-61, 1989  
 A;Title: Amino-acid sequence of the hinge region in chicken myosin subfragment-2.  
 A;Reference number: S02082; MUID:89228549; PMID:2713098  
 A;Accession: S02082  
 A;Molecule type: protein  
 A;Residues: 1144-1270 <WAT>  
 R;Yajima, E.  
 Nagasaki, Igakkaishi Zasshi 65, 409-430, 1990  
 A;Title: Study on tail region of skeletal muscle myosin: primary structure and protease  
 A;Reference number: PW0009  
 A;Molecule type: protein  
 A;Residues: 1304-1938 <YAL>  
 R;Moore, L.A.; Arrizubietta, M.J.; Tidman, W.E.; Herman, L.A.; Bandman, E.  
 A;Description: Analysis of the chicken fast myosin heavy chain family: Localization of isoforms  
 A;Reference number: S39081  
 A;Molecule type: mRNA  
 A;Residues: 1081-1203, DV, 1206-1342, E, 1344-1544, S, 1546-1795, HV, 1798-1829, S, 1831  
 A;Cross-references: EMBL:M74084  
 R;Moore, L.A.; Arrizubietta, M.J.; Tidman, W.E.; Herman, L.A.; Bandman, E.  
 J. Mol. Biol. 225, 1143-1151, 1992  
 A;Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoforms  
 A;Reference number: S24348; MUID:92309413; PMID:1377278  
 A;Accession: S24351  
 A;Molecule type: mRNA  
 A;Residues: 1082-1182, T, 1184-1203, DV, 1206-1342, E, 1344-1544, S, 1546-1780, M, 1782-  
 A;Cross-references: EMBL:M74084  
 R;Watanabe, B.  
 Biol. Chem. Hoppe-Seyler 370, 1027-1034, 1989  
 A;Title: Complete amino-acid sequence of subfragment-2 in adult chicken skeletal muscle  
 A;Reference number: S05515; MUID:90121764; PMID:2610940  
 A;Accession: S05515  
 A;Molecule type: protein  
 A;Residues: 842-906, Q, 908-1270 <WA3>  
 R;Watanabe, B.  
 Biol. Chem. Hoppe-Seyler 370, 549-558, 1989  
 A;Title: Amino-acid sequence of the short subfragment-2 in adult chicken skeletal muscle  
 A;Reference number: S04501; MUID:89374003; PMID:2775482  
 A;Accession: S04501  
 A;Molecule type: protein  
 A;Residues: 852-906, Q, 908-1108 <WA2>  
 R;Matsuda, G.; Maita, T.; Miyanishi, T.; Hayashida, M.  
 J. Protein Chem. 6, 33-46, 1987  
 A;Title: Structure and function of muscle myosin.  
 A;Reference number: A60877  
 A;Accession: A60877  
 A;Molecule type: protein  
 A;Residues: 1-139, 141-205 <MA1>  
 R;Guilick, J.; Kropp, K.; Robbins, J.  
 J. Biol. Chem. 260, 14513-14520, 1985

A;Title: The structure of two fast-white myosin heavy chain promoters. A comparative study  
 A;Reference number: A92507; MUID:86033956; PMID:2997212  
 A;Accession: A92507  
 A;Molecule type: DNA  
 A;Residues: 'M', 1-168 <GUL>  
 A;Cross-references: GB:ML12; GB:ML2083; GB:ML13510; NID:9212363; PIDN:AA48966\_1; PID:9  
 R;Kropp, K.; Gulick, J.; Robbins, J.  
 J. Biol. Chem. 261, 6613-6618, 1986  
 A;Title: A canonical sequence organization at the 5'-end of the myosin heavy chain genes  
 A;Reference number: A92587; MUID:86196091; PMID:3009465  
 A;Accession: C25217  
 A;Molecule type: DNA  
 A;Residues: M, 1-56, T, 58-76, I, 78-168 <KRO>  
 A;Cross-references: GB:ML13515; GB:ML1511; NID:212373; PIDN:AAA48971\_1; PID:9555468  
 C;Comment: This is a fragment of the globular head.  
 C;Superfamily: myosin heavy chain; myosin motor domain homology  
 C;Keywords: acetylated amino end; actin binding; ATP; coiled coil; hydrolase; methylated  
 F;1-1988/Region: myosin motor domain homology <MMOT>  
 F;179-186/Region: nucleotide-binding motif A (P-loop)  
 F;50-587/Region: actin binding #status predicted  
 F;657-679/Region: actin binding #status predicted  
 F;841-1289/Region: S2  
 F;852-1108/Region: short subfragment 2 <SPB2>  
 F;1290-1938/Region: light meromyosin  
 F;1;Modified site: acetylated amino end (Nla) #status experimental  
 F;35/Modified site: NG-methyllysine (Lys) #status experimental  
 F;130, 551/Modified site: NG,N6-trimethyl-Lysine (Lys) #status experimental  
 F;697, 707/Active site: Cys #status predicted  
 F;755/Modified site: 3'-methylhistidine (His) #status experimental  
 F;1  
 Query Match  
 Best Local Similarity 24.6%; Score 63.5; DB 1; Length 1938;  
 Matches 18; Conservative 13; Mismatches 7; Indels 11; Gaps 3;  
 QY 9 KCQRIQIENELLINEVALQVDRKVA-DEE---KOSYDAVVATVIST 51  
 ||| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 1559 KILKQLEINQKSE----IDRKIAEDEEDQPLKRHRIVESMQST 1602

RESULT 11  
 F64956  
 hypothetical protein HP0614 - Helicobacter pylori (strain 26695)  
 C;Species: Helicobacter pylori  
 C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
 C;Accession: F64956  
 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Kblak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997  
 A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.M.; Reference number: S05515; MUID:90121764; PMID:2610940  
 A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
 A;Reference number: A64520; MUID:97394467; PMID:9252185  
 A;Accession: F64596  
 A;Molecule type: DNA  
 A;Residues: 1-111 <TOM>  
 A;Accession: F64596  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Cross-references: UNIPROT:O25315; GB:AE000576; PIDN:AA07681  
 C;Superfamily: Helicobacter pylori hypothetical protein jhp0557  
 Query Match 24.4%; Score 63; DB 2; Length 111;  
 Best Local Similarity 40.6%; Pred. No. 4;  
 Matches 13; Conservative 8; Mismatches 11; Indels 0; Gaps 0;  
 QY 11 ORLOEMMELNEVAYALQVDRKVADEBEKOSYD 42  
 ||| :||:||:||:||:||:||:||:||:  
 Db 12 QALQAKRKULTELAELABIKVSSRFSPN 43

RESULT 12  
 EB4283



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GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: November 3, 2005, 21:37:29 ; Search time 93.246 Seconds  
(without alignments)  
291.060 Million cell updates/sec

Title: 09782816-52  
Perfect score: 258

Sequence: 1 GEKETPVQKCQLQIENEL.....ADEEKQSYDAVATVISTAR 53

Scoring table: BLASTM62

Gapop 10 0 , Gapext 0.5

Searched:

1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03;\*  
1: uniprot\_sprot;\*  
2: uniprot\_trembl;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %	Match Length	DB ID	Description
1	243.5	94.4	380	2 Q9V4Y9	Q9V4Y9 drosophila
2	127.5	49.4	388	2 QTPZ25	QTPZ25 anophelles g
3	82	31.8	402	2 Q9PTG6	Q9PTG6 gallus galli
4	77	29.8	242	2 Q6CYKL	Q6CYKL erwinia car
5	75	29.1	405	2 Q7T3H1	Q7T3H1 brachydanio
6	74	28.7	401	1 QDT2_MOUSE	QDT2_MOUSE mus musculus
7	74	28.7	402	1 Q6AYH5	Q6AYH5 rattus norvegicus
8	73.5	28.5	403	2 Q66J30	Q66J30 xenopus lae
9	72.5	28.1	400	1 QDT2_HUMAN	QDT2_HUMAN homo sapien
10	70.5	27.3	403	2 Q6IRB3	Q6IRB3 xenopus lae
11	70.5	27.3	755	2 Q9LNM1	Q9LNM1 arabidopsis
12	70.5	27.3	879	2 Q9YHDB	Q9YHDB rana catesbeiana
13	70.5	27.3	1937	1 MYH8_HUMAN	MYH8_HUMAN homo sapien
14	69.5	26.9	230	2 Q9DT99	Q9DT99 listeria in
15	68	26.4	297	2 Q9YDK9	Q9YDK9 aeropyrum p
16	67.5	26.2	162	1 Y157_AQUAE	Y157_AQUAE aquiflex aeo
17	67.5	26.2	338	2 Q7ZXY2	Q7ZXY2 xenopus lae
18	67.5	26.2	1939	2 Q6DFO6	Q6DFO6 xenopus lae
19	66	25.6	480	2 Q8H1NS	Q8H1NS arabidopsis
20	66	25.6	508	2 Q7XJBQ	Q7XJBQ arabidopsis
21	65.5	25.4	1935	2 Q6N3X3	Q6N3X3 xenopus tro
22	65	25.2	730	1 YE45_SCHEPO	YE45_SCHEPO schizosaccharomyces pombe
23	64.5	25.0	157	1 Q9PK98	Q9PK98 chlamydia m
24	64.5	25.0	935	2 Q81734	Q81734 trypanosoma
25	64	24.8	886	1 RAS0_SULAC	RAS0_SULAC sulfolobus
26	63.5	24.6	657	2 Q8ISE9	Q8ISE9 spirillum
27	63.5	24.6	63	2 Q91208	Q91208 oncorynchus
28	63.5	24.6	708	2 Q9YHD7	Q9YHD7 rana catesbeiana
29	63.5	24.6	826	2 Q9YHDS	Q9YHDS rana catesbeiana
30	63.5	24.6	1084	1 MYSS_RABIT	MYSS_RABIT oryzolagrus
31	63.5	24.6	1937	2 Q8JIP5	Q8JIP5 oncorhynchus

32 63.5 24.6 1938 1 MYSS\_CHICK  
33 63.5 24.6 1941 1 MYH2\_HUMAN  
34 63.5 24.6 1941 1 Q86T56 homo sapien  
35 63.5 24.6 2664 2 Q7RELO plasmoidium  
36 63 24.4 111 2 025335 helicobacte  
37 63 24.4 207 2 Q983X1 rhizobium 1  
38 63 24.4 716 2 Q46317 carnobacter  
39 63 24.4 716 2 Q9REY3 carnobacter  
40 62.5 24.2 45 2 Q71IU8 lactobacillus  
41 62.5 24.2 222 2 Q9HQ83 halobacteri  
42 62.5 24.2 469 2 Q9BSW6 mus musculus  
43 62.5 24.2 892 2 Q63939 ratus sp.  
44 62.5 24.2 1119 2 P87344 theragra ch  
45 62.5 24.2 1725 2 Q7RT66 plasmoidium

## ALIGNMENTS

RESULT 1  
Q9V4Y9 PRELIMINARY; PRT; 380 AA.  
ID Q9V4Y9;  
AC Q9V4Y9;  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
DB CG8269+PA (LDD07949P).  
GN Name=DMM; ORFnames=CG8269;  
OS Drosophila melanogaster (fruit fly).  
OC Buxaroya; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Dictyota; Diptera; Hymenoptera;  
OC Ephdroidea; Drosophilidae; Drosophila;  
RN NCBI-TaxID=7227;

[1]  
RP SEQUENCE FROM N.A.  
MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Cainiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scheer S.E., Li P.W., Hoskink R.A., Gille R.F.,  
RA George R.A., Lewis S.E., Richards S.E., Ashburner M., Henderson S.N.,  
RA Sutton G.J., Wortman J.R., Brandt M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.I.,  
RA Abril J.F., Agbayani A., An H.J., Andrews P., Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolnsakov S.,  
RA Borrova M.J., Bouck J., Brokstein P., Brottier P.,  
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra T.,  
RA Cherry J.M., Cawley S., Dahlke B., Daveyport L.B., Davies P.,  
RA De Pablo J., Delcher A., Dew Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Douc L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferrazzi C., Ferreira S., Fleischmann W.,  
RA Fosler C., Gabrelien A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman R.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibeagwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milashina N.V., Mobarry C., Morris J., Mosherfi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nussekern D.R., Pacleb J.M.,  
RA Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler P., Shen H.,  
RA Shue B.C., Sieden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
RA Merkulov G., Milashina N.V., Mobarry C., Morris J., Mosherfi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nussekern D.R., Pacleb J.M.,  
RA Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler P., Shen H.,  
RA Shue B.C., Sieden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wasman D.A., Weinstock G.M., Weissenbach J.,  
RA Williams S.M., Woodager C., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195 (2000).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426065; PubMed=12537568;  
 RA Celinker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champé P., Dugan S., Prise E., Hodgson A.,  
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,  
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svartkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*  
 RT melanogaster euchromatic genome sequence";  
 RL Genome Biol. 3:RESEARCH0079, RESEARCH0079(2002).  
 RN [13]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svartkas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celinker S.E.,  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RA a genomic perspective";  
 Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [14]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bernan B.P.,  
 RA Bettencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 systematic review";  
 Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
 RN [15]  
 RP SEQUENCE FROM N.A.  
 RG FLYBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN [16]  
 RP SEQUENCE FROM N.A.  
 RG FLYBase;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 RN [17]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkely;  
 RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,  
 RA Champé P., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mongallic C.J.,  
 RA Nuño J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celinker S.,  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE00385; AAH59034.1; --.  
 DR EMBL; AY061092; AAC28640.1; --.  
 DR Intact; Q9V4Y9; --.  
 DR FlyBase; FBgn0021835; Dmnp.  
 GO; GO:0005869; C: dynactin complex; IEA.  
 GO; GO:0070107; P: microtubule-based process; IEA.  
 DR InterPro; IPR06956; Dynamitin.  
 DR Pfam; PF04912; Dynamitin; 1.  
 SQ SEQUENCE 380 AA; 41998 MW; CPE1D3BPF5999C5 CRC64;

Query Match 94.4%; Score 243.5; DB 2; Length 380;  
 Best Local Similarity 98.1%; Pred. No. 1e-18;  
 Matches 52; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GEKETPVOKCQRIQIEMMELNEVALQVDRKVADEEQSYDAVVATVSTAR 53  
 DR 94 GEKETPVOKCQRIQIEMMELNEVALQVDRKVADEEQSYDAVVATVSTAR 145

ID Q7P225 PRELIMINARY; PRT; 388 AA.  
 AC Q7P225;  
 DT 01-MAR-2004 (Tremblrel. 26, Created)  
 DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE ASGP951 (Fragment)  
 GN Name=AGC052050; ORFNames=ENSANGG00000015420;  
 OS Anopheles gambiae str. PEST.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.  
 OC NCBITaxID=180454;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EST;  
 RA Anopheles Genome Sequencing Consortium;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 CC -- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AAAB01008986; EA00075.1; --.  
 GO; GO:0005859; C: dynactin complex; IEA.  
 DR GO:0007017; P: microtubule-based process; IEA.  
 DR InterPro; IPR06936; Dynamitin.  
 DR Pfam; PF04912; Dynamitin; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 388 AA; 4F5A549B51D52555 CRC64;  
 DR Query Match 49.4%; Score 127.5; DB 2; Length 388;  
 DR Best Local Similarity 49.1%; Pred. No. 7.5e-06;  
 DR Matches 26; Conservative 11; Mismatches 15; Indels 1; Gaps 1;  
 DR Non\_TER 1 1  
 DR 1 GEKETPVOKCQRIQIEMMELNEVALQVDRKVADEEQSYDAVVATVSTAR 53  
 DR 94 GEKETPVOKCQRIQIEMMELNEVALQVDRKVADEEQSYDAVVATVSTAR 145

RESULT 3

ID	Q9PTG6	PRT;	PRT;	PRT;
ID	Q9PTG6	PRELIMINARY;	PRT;	402 AA.
AC	Q9PTG6;			
DT	01-MAY-2000 (Tremblrel. 13, Created)			
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)			
DT	01-MAR-2003 (Tremblrel. 23, Last annotation update)			
DE	Dynamitin.			
GN	Name=p50;			
OS	Gallus gallus (Chicken)			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
OC	NCBI_TaxID=9031;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20056093; PubMed=10598646;			
RA	Valetti C., Wetzel D.M., Schrader M., Hashani M.J., Gill S.R., Kreis T.F., Schröer T.A.;			
RA	"Role of dynactin in endocytic traffic: effects of dynamitin overexpression and colocalization with CLIP-170.", Mol. Biol. Cell 10:4107-4120(1999).			
RA	[2]			
RP	SEQUENCE FROM N.A.			
RA	Schröer T.A., Gill S.R., Hashani J., Crego C.;			
RA	Schröer T.A., Gill S.R., Hashani J., Crego C.;			
RA	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
DR	AF00774; AF13936.1; --.			
DR	GO; GO:0005859; C: dynactin complex; IEA.			
DR	GO; GO:0007017; P: microtubule-based process; IEA.			
DR	InterPro; IPR06936; Dynamitin.			
DR	Pfam; PF04912; Dynamitin; 1.			
SQ	SEQUENCE 402 AA; 45126 MW; F229C467C630DCB9 CRC64;			
DR	Query Match 31.8%; Score 82; DB 2; Length 402;			
DR	Best Local Similarity 48.7%; Pred. No. 0.86; Mismatches 12; Indels 2; Gaps 1;			

RESULT 2

Q7P225.

QY	1 GEKETPVOKCQRCIEMNELLNEVALO--VDRKVADEEB	37	RA	Villalon D.K., Muñiz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
ID	Q6CYK1	PRELIMINARY;	PRT;	Fahay J., Heitton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
AC	Q6CYK1;			Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G.,
DB	96 GAKETPVOKCQRCIEMNELLNEVALO--VDRKVADEEB	134	RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
			RA	Rodriguez A.C., Grimeswood J., Schmitz J., Myers R.M., Butterfield Y.S.,
			RA	Krzewinski M.I., Skalska U., Smalius D.E., Schneich A., Schein J.B.,
			RA	Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
			RT	and mouse cDNA sequences";
			RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
			RN	[2]
			RP	SEQUENCE FROM N.A.
			RC	TISSUE=Embryo;
			RA	Strausberg R.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
			RL	EMBL: BC053120; RAH53120.1; -;
			DR	ZFIN; ZIB_GENE_09426-1279; ZGC:63867;
			DR	GO; GO:0005809; Cdc42nactin complex; IEA.
			GO	GO:0007017; R-microtubule-based process; IEA.
			DR	InterPro; IPR005996; Dynamitin.
			DR	Pfam; PP04912; Dynamitin_1.
			SG	SEQUENCE 405 AA; 44638 MW; CA00047342500953 CRC64;
			QY	Query Match 29.8%; Score 77; DB 2; Length 242; Best local similarity 40.9%; Pred. No. 1.8; Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
			DR	Query Match 29.1%; Score 75; DB 2; Length 405; Best local similarity 43.6%; Pred. No. 5.2; Matches 17; Conservative 7; Mismatches 15; Indels 0; Gaps 0;
			Db	1 GEKETPVOKCQRCIEMNELLNEVALO--VDRKVADEEB
			QY	4 ETPVOKCQQLQIENMELNEVAALQDRKVADEEBQ 39
			DR	96 GAKETPVOKCQRCIEMNELLNEVALO--VDRKVADEEB
			SG	Name=DCCn2;
			OC	Mus musculus (Mouse)
			OC	Bivalvia; Emetozoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus; Metazoa; Rodentia; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
			OX	NCBI_TaxID=10090;
			RN	[1]
			RP	SEQUENCE FROM N.A.
			RX	MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
			RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
			RA	Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
			RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Ronald M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Rana S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muniz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahay J., Heitton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.N., Krzewinski M.I., Skalska U., Smalius D.E., Schneich A., Schein J.B., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
			RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
			RN	[2]
			RP	SEQUENCE OF 65-74; 77-91; 102-116; 156-170; 194-216 AND 309-320; SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.

RC TISSUE=Brain; PubMed=9144527; DOI=10.1006/bbrc.1997.6447;  
 RX MEDLINE=97289622; PubMed=9144527; DOI=10.1006/bbrc.1997.6447;  
 RA Abe T.K., Tanaka H., Iwanaga T., Odani S., Kuwano R.;  
 RT "The presence of the 50-kDa subunit of dynein complex in the nerve  
 growth cone.";  
 RL Biochem. Biophys. Res. Commun. 233:295-299(1997).  
 RN [3]  
 RP INTERACTION WITH BICD2.  
 RX MEDLINE=2137652; PubMed=11493508; DOI=10.1093/embj/20.15.4041;  
 RA Hoogenraad C.C., Althamova A., Howell S.A., Dordland B.R.,  
 RA de Zeeuw C.I., Willemsen R., Visser P., Grosveld F., Galjart N.;  
 RT "Mammalian Golgi-associated Bicaudal-D2 functions in the dynein-  
 dynein pathway by interacting with these complexes.";  
 RL EMBO J. 20:4041-4054 (2001).  
 CC --!- SUBUNIT: Subunit of dynein, a multiprotein complex associated  
 CC with dynein (BY SIMILARITY). Interacts with BICD2.  
 CC --!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.  
 CC --!- DEVELOPMENTAL STAGE: Present at high levels in both cytoplasmic  
 CC and membrane-associated forms in neurons. Levels of membrane-  
 CC associated form are greatly reduced in the adult.  
 CC  
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 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to license@isb-sib.ch).  
 DR EMBL; BC004613; AAC04613.1; -.  
 DR MGI; MGI\_10773; Dctn2.  
 DR InterPro; IPR06996; Dynamin.  
 DR Pfam; PF04912; Dynaminin.  
 KW Coiled coil; Cytoskeleton; Direct protein sequencing; Dynein;  
 KW Membrane; Microtubule; Motor protein.  
 FT INIT MET 0 By similarity.  
 FT DOMAIN 98 131 Coiled coil (Potential).  
 FT DOMAIN 214 244 Coiled coil (Potential).  
 SEQUENCE 401 AA; 43985 MW; 153E4AABD5940BBC CRC64;  
 Query Match 28.7%; Score 74; DB 1; Length 401;  
 Best Local Similarity 35.8%; Pred. No. 6.6;  
 Matches 19; Conservative 10; Mismatches 24; Indels 0; Gaps 0;  
 QY 1 GEKETPVOKQORLDEMNLNEVAIQLQDRVKYADEEKOSYDAVVATVSTAR 53  
 Db 94 GVKEETPQOKYOKRLHEVEQDLTTEVKIKTVKOSATEKLTPVVLAKQDAALK 146  
 Query Match 28.7%; Score 74; DB 2; Length 402;  
 Best Local Similarity 35.8%; Pred. No. 6.7;  
 Matches 19; Conservative 10; Mismatches 24; Indels 0; Gaps 0;  
 RESULT 7  
 Q6A7H5 PRELIMINARY; PRT; 402 AA.  
 ID Q6A7H5; PRELIMINARY; PRT; 403 AA.  
 DT 25-OCT-2004 (TREMBrel. 28, Created)  
 DT 25-OCT-2004 (TREMBrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBrel. 28, Last annotation update)  
 DE Name=MGB2128; GN Name=MGB2128;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 NCBI\_TaxID=8355; RN [1]  
 RN RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney; PubMed=12341132; DOI=10.1002/dvdy.10174;  
 RX MEDLINE=22341132; PubMed=12341132; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative.";  
 RL Dev. Dyn. 225:384-391(2002).  
 RN Name=Dctn2;  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strasberg R.L., Feingold E.A., Wagner L., Shemesh C.M., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Brat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McCowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzyk D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Heitton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,  
 RA Kuziwinski M.I., Skalska U., Smailus D.E., Schein J.E.,  
 RA Jonas S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RA Director MGC Project;  
 RL Submitted (Aug-2004) to the EMBL/GenBank/DDJB databases.  
 DR EMBL; BC079042; AAC79042.1; -.  
 GO; GO:0005859; P:microtubule-based process; IEA.  
 DR InterPro; IPR06936; Dynamin.  
 DR Pfam; PF04912; Dynaminin\_1.  
 SQ SEQUENCE 402 AA; 44148 MW; 55033535A4PB052 CRC64;  
 Query Match 28.7%; Score 74; DB 2; Length 402;  
 Best Local Similarity 35.8%; Pred. No. 6.7;  
 Matches 19; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.N.,  
 RA Fahey J., Heitman E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J., Schmitz J., Myers R.M., Butterfield Y.S.,  
 RA Rodriguez A.C., Grinwood J., Schmitz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.B., Schnurch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RL [3]  
 RN RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Klein S., Gerhard D.S.; Submitted (AUG-2004) to the EMBL/GenBank/DDJB databases.  
 RL DR EMBL; BCB081081; AAM81081.1; -  
 DR Pfam; PRO4912; Dynamitin; 1;  
 SQ SEQUENCE 403 AA; 44737 MW; 868E8CEB54325EP3 CRC64;  
 Query Match 28.5%; Score 73.5; DB 2; Length 403;  
 Best Local Similarity 45.1%; Pred: 7.6; Mismatches 5; Indels 22; Gaps 1;  
 Matches 23; Conservative 5;  
 Qy 1 GKEKTPVQKQRLQIEMMELINNEVALQ-VDRKVADEEKKRKYDAWATVIS 50  
 94 GMKMKTPQKQYQRLHENVQLTQEVEKTQSTWVKSAEKKLTPVALAKQVAS 144  
 RESULT 9  
 DCT2\_HUMAN STANDARD; PRT; 400 AA.  
 ID DCT2\_HUMAN STANDARD; PRT; 400 AA.  
 AC O13561; 086YMN2; Q2BW17;  
 DT 01-NOV-1997 (Rel. 35; Created)  
 DT 05-JUL-2004 (Rel. 44; Last annotation update)  
 DE Dynactin complex 50-kDa subunit (50 kDa dynein-associated polypeptide)  
 DE (p50 dynein) (DCTN-50) (Dynactin 2).  
 GN Name=DCTN2; Synonyms=DCTN50;  
 OS Homo sapiens (Human);  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 RN [1] NCBI\_TaxID:9606;

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RA MEDLINE-9617072, PubMed-8647893; DOI-10.1083/jcb.132.4.617;  
 RA Echeverri C.J., Paschall B.M., Vaughan K.T., Vallee R.B.;  
 RT "Molecular characterization of the 50-kD subunit of dyneactin reveals  
 RT function or the complex in chromosome alignment and spindle  
 organization during mitosis"; J. Cell Biol. 132:617-633 (1996).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Placenta; Skin; and uterus;  
 RC MEDLINE-2238257; PubMed-12479732; DOI-10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shearman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K., Schaefer C.P., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Matsuda K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bondo M.R., Caavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Usdin T.B., Iosifuki S., Carninci P., Prange C.,  
 RA Ratai S.S., Loquelandio N.A., Peters G.J., Abramson R.D., Millahy S.J.,  
 RA Borak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Heitman E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grinwood J., Schmitz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,

RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RL [3]  
 RN SEQUENCE OF 1-384 FROM N.A.  
 RA Aumais J.P., Yu-Lee L.Y.; "Human 50 kd dynein subunit, p50 dynamitin, isolated from HeLa  
 RT cells"; Submitted (NOV-2002) to the EMBL/GenBank/DDJB databases.  
 RL [4]  
 RN SEQUENCE OF 1-131.  
 RC TISSUE=Platelet;  
 RX MEDLINE-22608398; PubMed-12665801; DOI-10.1038/nbt810;  
 RA Gevaert K., Goethals M., Martens L., Van Damme J., Staels A.,  
 RA Thomas G.R., Vandekerckhove J.; "Exploring proteomes and analyzing protein processing by mass  
 RT spectrometric identification of sorted N-terminal peptides"; Nat. Biotechnol. 21:566-569 (2003).  
 CC C:kinetochore; C:cytoskeleton; C:cell proliferation; C:cell cycle; C:chromosome alignment and spindle  
 CC organization during mitosis. May play a role in synapse formation  
 CC during brain development  
 CC -!- SUBUNIT: Subunit of dynein, a multiprotein complex associated  
 CC with dynein.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.  
 CC ---  
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 CC ---  
 DR EMBL; U50733; AAC50423.1; -  
 DR EMBL; BC000718; AAM00718.1; -  
 DR EMBL; BC009469; AAM09469.1; -  
 DR EMBL; BC014083; AAM14083.1; -  
 DR EMBL; AY189155; AM034395.1; -  
 DR Genew; HGNC:2712; DCTN2.  
 DR MM; 617376; -  
 DR GO; GO:0005813; C:centrosome; TAS.  
 DR GO; GO:0005869; C:dynein complex; TAS.  
 DR GO; GO:000776; C:kinetochore; TAS.  
 DR GO; GO:0008283; C:cell proliferation; TAS.  
 DR GO; GO:0007067; P:mitosis; TAS.  
 DR InterPro; IPR006956; Dynamitin.  
 DR Pfam; PRO4912; Dynamitin; 1;  
 KW Coiled coil; Cytoskeleton; Direct protein sequencing; Dynein;  
 KW Membrane; Microtubule; Motor protein.  
 FT INIT MET 0  
 FT DOMAIN 98 131 Coiled coil (Potential).  
 FT DOMAIN 213 243 Coiled coil (Potential).  
 FT DOMAIN 378 398 Coiled coil (Potential).  
 FT CONFLICT 34 34 A -> ARQQL (in Ref. 1).  
 FT CONFLICT 35 35 E -> BLE (in Ref. 3).  
 FT CONFLICT 381 384 LATV -> PGHS (in Ref. 3).  
 SQ SEQUENCE 400 AA; 4499 MW; 085AG85C08270F CRC64;  
 Query Match 28.1%; Score 72.5; DB 1; Length 400;  
 Best Local Similarity 48.7%; Pred No. 9.7; Mismatches 14; Indels 1; Gaps 1;  
 Matches 19; Conservative 5; Mismatches 14; Indels 1; Gaps 1;  
 Qy 1 GKEKTPVQKQRLQIEMMELINNEVALQD-RKYADEK 38  
 DB 93 GVKEKTPQKQYQRLHENVQLTTEVEKIKIVKESATEK 131  
 RESULT 10  
 ID Q6TRB3  
 ID Q6TRB3 PRELIMINARY; PRT; 403 AA.  
 AC Q6TRB3;

DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DB Dctn2-prov protein.  
 GN Name=dctn2-prov;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,  
 RA Blatchenko L., Marusina K., Farmer A.A., Robin G.M., Hong L.,  
 RA Steapleton M., Soates M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loqueillan N.A., Peters G.J., Abramson R.D., Mulahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Murny D.M., Sodergren S.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton B., Yettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green D., Dickson M.C.,  
 RA Rodiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalius D.E., Schnarch J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RP [2]  
 RC TISSUE=Embryo;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.I., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RT Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative";  
 RL Dev. Dyn. 225:384-391 (2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RA Klein S., Strausberg R.;  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC070987; AAH70987\_1; -.  
 DR GO; GO:0005889; C-dynactin complex; IEA.  
 DR GO; GO:0007017; P-microtubule-based process; IEA.  
 DR InterPro; IPR0063996; Dynamin.  
 DR Pfam; PF04912; Dynamin\_1.  
 SQ SEQUENCE 403 AA; 44838 MW; 9F0158C7C7983062 CRC64;

RESULT 11  
 Q9YH8I PRELIMINARY; PRT; 755 AA.

Query Match 27.3%; Score 70.5; DB 2; Length 403;  
 Best Local Similarity 51.3%; Pred. No. 16;  
 Matches 20; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

OY 1 GEKEKTPVQKQQLQTEMNELLNEVALQVD-RKVADEEK 38  
 94 GIKEKTPQQKTYQRLLHEVQELTQEVEKTQSILKESATEEK 132

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicoyledons; core eudicots; rosids;  
 OC euroids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,  
 RA Kim C., Altafi H., Bei Q., Chin C., Chiu J., Choi E., Conn L.,  
 RA Conway A., Gonzales A., Hansen N., Hawing B., Koo T., Lam B., Lee J.,  
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,  
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,  
 RA Toriumi M., Vaysberg M., Yu G., Federer Spiel N.A., Theologis A.,  
 RA Ecker J.R.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Cheuk R., Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,  
 RA Khan S., Kim A., Altafi H., Bei B., Chin C., Chiu J., Choi E., Lam B.,  
 RA Conn L., Conway A., Gonzalez A., Hansen N., Hawing B., Koo T., Lam B.,  
 RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,  
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,  
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federer Spiel N.,  
 RA Theologis A., Ecker J.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AAC023279; AF079274\_1; -.  
 DR InterPro; IPR001005; Myb\_DNA\_binding.  
 DR PROSITE; PS00037; MYB\_1; UNKNOWN 1.  
 SQ SEQUENCE 755 AA; 83720 MW; BADBCB41020E022A CRC64;

Query Match 27.3%; Score 70.5; DB 2; Length 755;  
 Best Local Similarity 38.5%; Pred. No. 31;  
 Matches 20; Conservative 9; Mismatches 16; Indels 7; Gaps 2;

OY 2 EKETPQKQQLQTEMNELLNEVALQVD-RKVADEEK 53  
 DB 582 EAEERIOQAER---EKNRAISEAAKAEER---EERGRDSEVARAQTR 626

RESULT 12  
 Q9YH8P PRELIMINARY; PRT; 879 AA.

ID Q9YH8P  
 ID Q9YH8B PRELIMINARY; PRT; 879 AA.

AC 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Myosin heavy chain (Fragment).  
 GN Name=MHC-1;  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=tail muscle;  
 RX MEDLINE=99179235; PubMed=10079518;  
 RX DOI=10.1002/(SICI)1520-6408(1999)24:1/2<151::AID-DVGI4>3..CO;2-W;  
 RA Hu H., Merrifield P., Atkinson B.G.;  
 RT "Expression of the myosin heavy chain genes in the tail muscle of  
 RT thyroid hormone-induced metamorphosing Rana catesbeiana tadpoles.";  
 RL Dev. Genet. 24:151-164(1999).  
 DR EMBL; AA097904; AA013769\_1; -.  
 DR HSSP; P25054; 1DEB.  
 DR GO; GO:0016459; C-myosin; IEA.  
 DR GO; GO:0003774; F-motor activity; IEA.  
 DR InterPro; IPR002928; Myosin-tail.  
 DR InterPro; IPR00533; Tropomyosin.  
 DR Pfam; PF01576; Myosin tail\_1; 1.  
 DR PRINTS; PRO0194; TROPOMYOSIN.  
 FT NON\_TER 1  
 SQ SEQUENCE 879 AA; 101710 MW; IC456851E968A3DB CRC64;

Query Match 27.3%; Score 70.5; DB 2; Length 879;  
 Best Local Similarity 36.8%; Pred. No. 36;

Matches	21;	Conservative	11;	Mismatches	14;	Indels	11;	Gaps	3;
Oy	1	GEKEFVPVKQRCQLQEMNELLNEVALQYDRKVA-DEE---KOSYDAVWTIVST	51	CC	-!- DOMAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils.				
Db	489	GSLEHEESKILRQIOLNQSE----YRKIAKDEEEQLKNSQRDITDMOST	540	CC	-!- DISEASE: Defects in MYH8 are a cause of Carney complex variant [IMM:608937]. Carney complex is a multiple neoplasia syndrome characterized by spotty skin pigmentation, cardiac and other myxomas, endocrine tumors, and psammomatous melanotic schwannomas.				
				CC	Familial cardiac myxomas are associated with spotty pigmentation of the skin and other phenotypes, including primary pigmented nodular adrenocortical dysplasia, extracardiac (frequently cutaneous) myxomas, schwannomas, and pituitary, thyroid, testicular, bone, ovarian, and breast tumors. Cardiac myxomas do not develop in all patients with the Carney complex, but affected patients have at least two features of the complex or one feature and a clinically significant family history.				
				CC	-!- DISEASE: Defects in MYH8 are a cause of trismus-pseudocampodactyly syndrome [IMM:158300]; also called Hecht-Beals or Dutch-Kentucky syndrome. The trismus-pseudocampodactyly syndrome is a hereditary distal arthrogryposis characterized by an inability to open the mouth fully (trismus) and inability to extend the fingers (pseudocampodactyly). The dominant trait produces involuntary flexion contracture of distal and proximal interphalangeal joints. Such hand and jaw contractures are caused by shortened flexor muscle-tendon units. Similar lower-limb contractures also produce foot deformity. The trismus-pseudocampodactyly syndrome is a morbid autosomal dominant trait with variable expressivity but high penetrance. In these patients, trismus complicates dental care, feeding during infancy, and intubation for anesthesia, and the pseudocampodactyly impairs manual dexterity, with consequent occupational and social disability. Many patients require surgical correction of contractures.				
				CC	-!- MISCELLANEOUS: Each myosin heavy chain can be split into 1 light meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be split further into 2 globular subfragments (S1) and 1 rod-shaped subfragment (S2).				
				CC	-!- SIMILARITY: Contains 1 IQ domain.				
				CC	-!- SIMILARITY: Contains 1 myosin-like globular head domain.				
				CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).				
				CC	-----				
				DR	EMBL: M36769; AAC17185.1; -.				
				DR	EMBL: Z28133; CAB62293.1; -.				
				DR	EMBL: X51592; CAB35941.1; -.				
				DR	EMBL: AR006713; AAC21557.1; -.				
				DR	PIR: I38055; I38055.				
				DR	HSSP: P3538; 2MYS.				
				DR	Genew: HNC:7578; MYH8.				
				DR	MIM: 160741; -.				
				DR	MIM: 608837; -.				
				DR	MIM: 158300; -.				
				DR	GO: GO:0005829; C: muscle myosin; TAS.				
	[6]	VARIANT CARNEY COMPLEX VARIANT/PRISMUS-PSEUDOCAMPODOACTYL SYNDROME		DR	GO: GO:0008307; F: structural constituent of muscle; TAS.				
		GLN-674.		DR	InterPro: IPR000168; IQ_resid.				
		PubMed:15282353; DOI=10.1056/NEJMoa040584;		DR	InterPro: IPR001049; Myosin_head.				
		RA		DR	InterPro: IPR002228; Myosin_tail.				
		Veugelers M., Bressan M., McDermott D.A., Wermowicz S., Morton C.C.,		DR	PFam: PF00612; IQ; 1.				
		RA		DR	PFam: PF0063; Myosin_head; 1.				
		Mahry C.C., Lefevre J.-F., Zunamon A., Desfrere A., Chaudron J.-M.,		DR	PFam: PF02736; Myosin_N; 1.				
		RA		DR	PFam: PF01576; Myosin_tail; 1.				
		Baobon C.T.,		DR	PRINTS: PR00193; MYOSINHEAVY.				
		RT		DR	ProDom: PD00355; Myosin_head; 1.				
		"Mutation of perinatal myosin heavy chain associated with a Carmey complex variant.";		DR	Prosite: PS50096; IQ; 1.				
		RT		KW	Actin-binding; Arp-binding; Calmodulin-binding; Coiled coil; Disease mutation; Methylation; Multigene family; Muscle protein; Myosin; Thick filament.				
		RL		KW	-!- SUBUNIT: Muscle myosin is a hexameric protein that consists of 2 heavy chain subunits (MHC), 2 alkali light chain subunits (MLC-2), and 2 regulatory light chain subunits (MLC-1).				
		N. Engl. J. Med. 351:460-469(2004).		KW	-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.				
CC	-!-								
CC	-!-								
CC	-!-								



OM protein - protein search, using sw model  
Run on: November 3, 2005, 21:51:39 ; Search time 27.2086 Seconds  
145.410 Million cell updates/sec

Title: 09782816-52  
Perfect score: 258  
Sequence: 1 GEREKTPVQVKCQLQIENEL.....ADEEKQSYDAWATVISTAR 53  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 513545 seqs, 74649064 residue

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
listing first 45 summaries

Database : Issued Patents All:  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:  
3: /cgn2\_6/ptodata/1/iaa/5C\_COMB.pep:  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:  
5: /cgn2\_6/ptodata/1/iaa/RETUS\_COMB.pep:  
5: /cgn2\_6/ptodata/1/iaa/backfile1.pep:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	160	62.0	142	4 US-09-270-767-43370
2	70.5	27.3	1937	4 US-09-538-092-918
3	62.5	24.2	1939	4 US-09-538-092-915
4	62.5	24.2	1939	4 US-09-949-016-11104
5	61.5	23.8	1939	4 US-09-949-016-6925
6	61.5	23.8	1942	4 US-09-949-016-8135
7	59.5	23.1	1940	4 US-09-538-092-901
8	59.5	23.1	1963	4 US-09-949-016-8888
9	58	22.5	1248	3 US-09-080-897-2
10	58	22.5	1255	2 US-09-080-897-4
11	58	22.5	1255	3 US-09-080-899-595-1
12	58	22.5	1255	3 US-09-323-735-4
13	58	22.5	1315	3 US-09-899-595-3
14	58	22.5	1413	4 US-09-252-991A-23627
15	58	22.5	203	4 US-09-711-164-436
16	57	22.1	221	3 PCT-US94-01149-15
17	57	22.1	304	5 PCT-US94-01149-5
18	57	22.1	304	5 PCT-US94-01149-57
19	57	22.1	304	5 PCT-US94-01149-57
20	57	22.1	585	2 US-08-453-848-11
21	57	22.1	585	3 US-09-169-027-11
22	57	22.1	586	2 US-08-453-848-19
23	57	22.1	586	3 US-09-169-027-19
24	57	22.1	589	2 US-08-453-848-13
25	57	22.1	589	3 US-09-169-027-13
26	57	22.1	592	2 US-08-453-848-17
27	57	22.1	592	3 US-09-169-027-17

RESULT 1  
US-09-270-767-43370  
; Sequence 43370, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NO: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 43370  
; LENGTH: 142  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; US-09-270-767-43370  
; Query Match 62.0%; Score 160; DB 4; Length 142;  
; Best Local Similarity 100.0%; Pred. No. 7.4e-15;  
; Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
; Qy 1 GEREKTPVQVKCQLQIENEL.....ADEEKQSYDAWATVISTAR 53  
; Db 111 GEREKTPVQVKCQLQIENEL.....ADEEKQSYDAWATVISTAR 142  
; RESULT 2  
; US-09-538-092-918  
; ; Sequence 918 Application US/09538092  
; ; Patent No. 6753314  
; ; GENERAL INFORMATION:  
; ; APPLICANT: Giot, Loic  
; ; APPLICANT: Mansfield, Traci A.  
; ; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
; ; FILE REFERENCE: 15966-542  
; ; CURRENT APPLICATION NUMBER: US/09/538,092  
; ; CURRENT FILING DATE: 2000-03-29  
; ; PRIORITY APPLICATION NUMBER: 60/127,352  
; ; PRIOR FILING DATE: 1999-04-01  
; ; PRIORITY APPLICATION NUMBER: 60/178,965  
; ; PRIOR FILING DATE: 2000-02-01  
; ; NUMBER OF SEQ ID NO: 1387  
; ; SOFTWARE: CurapatisSeqFormatter Version 0.9  
; ; SEQ ID NO: 918  
; ; LENGTH: 1937  
; ; TYPE: PRT  
; ; ORGANISM: Homo sapiens  
; ; FEATURE: misc\_feature  
; ; NAME/KEY: misc\_feature

; LOCATION: (0)..(0)  
; OTHER INFORMATION: Polypeptide Accession Number P13535  
; US-09-538-092-918

Query Match 27.3%; Score 70.5; DB 4; Length 1937;  
Best Local Similarity 28.9%; Pred. No. 1..1; 8; Indels 31; Gaps 4;  
Matches 22; Conservative 15; Mismatches 8; Indels 31; Gaps 4;

QY 2 EKETPVQKCO-----RLQIENNELNEVALQVDRKVA--DEE-- 37  
Db 1533 KQVQEKECBIQAALEEAESLEHEGKILQLELNQVKSE---VDRKIAEKDEID 1587

QY 38 -KQSYDAVAVATVIST 51  
Db 1588 OLKRNHTRVVETMOSST 1603

RESULT 3  
US 09-538-092-915  
Sequence 915, Application US/09538092  
Patent No. 6753314

GENERAL INFORMATION:

APPLICANT: Giot, Loic  
APPLICANT: Mansfield, Traci A.  
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

PRIOR APPLICATION NUMBER: 6/0/127,352

PRIOR FILING DATE: 1999-04-01

PRIOR APPLICATION NUMBER: 6/0/178,965

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CuraPatSeqFormatter Version 0.9  
SEQ ID NO 915  
LENGTH: 1939  
TYPE: PRT  
ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY: misc\_feature

LOCATION: (0)..(0)

OTHER INFORMATION: Polypeptide Accession Number P12882  
US-09-538-092-915

Query Match 24.2%; Score 62.5; DB 4; Length 1939;  
Best Local Similarity 32.7%; Pred. No. 15; 8; Indels 11; Gaps 4;  
Matches 16; Conservative 14; Mismatches 8; Indels 11; Gaps 4;

QY 9 KCQRQIQLIEMELNLNEVALQVDRKVA-----DEEKQSYDAVAVATVIST 51  
Db 1561 KILRIOLELNQVKSE---VDRKIAEKDEIDOMKRNRHIVVESMOST 1604

RESULT 4  
US-09-949-016-1104  
Sequence 11104, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 6/0/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 6/0/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 6/0/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11104

RESULT 5  
US-09-949-016-6925  
Sequence 6925, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 6/0/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 6/0/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 6/0/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6925

LENGTH: 1939  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-6925

Query Match 23.8%; Score 61.5; DB 4; Length 1939;  
Best Local Similarity 36.7%; Pred. No. 21; 7; Indels 11; Gaps 3;  
Matches 18; Conservative 13; Mismatches 7; Indels 11; Gaps 3;

QY 9 KCQRQIQLIEMELNLNEVALQVDRKVA--DEE---KQSYDAVAVATVIST 51  
Db 1561 KILRIOLELNQVKSE---VDRKIAEKDEIDOMKRNRHIVVESMOST 1604

RESULT 6  
US-09-949-016-8135  
Sequence 8135, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 6/0/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 6/0/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 6/0/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8135

LENGTH: 1942  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-8135

Query Match 23.8%; Score 61.5; DB 4; Length 1942;  
 Best local Similarity 36.7%; Pred. No. 21; Mismatches 7; Indels 11; Gaps 3;  
 Matches 18; Conservative 13; Mismatches 7; Indels 11; Gaps 3;

Qy 9 KCQRQIEMNELLNEVALQVDRKVA--DRE---KQSVDAAWATVIS 51  
 Db 1564 KILRIOLELNQVKSE----IDRKIAEKDEBDOLKRNHLRVVBSMQST 1607

RESULT 7 US-09-538-092-901  
 Sequence 901, Application US/09538092  
 Patent No. 675314  
 GENERAL INFORMATION:  
 APPLICANT: Giot, Loic  
 APPLICANT: Mansfield, Traci A.  
 TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
 FILE REFERENCE: 15966-542  
 CURRENT APPLICATION NUMBER: US/09/538,092  
 CURRENT FILING DATE: 2000-03-29  
 PRIOR APPLICATION NUMBER: 6/127,352  
 PRIOR FILING DATE: 1999-04-01  
 PRIOR APPLICATION NUMBER: 6/178,965  
 PRIOR FILING DATE: 2000-02-01  
 NUMBER OF SEQ ID NOS: 1387  
 SOFTWARE: CurapatSeqFormatter Version 0.9  
 SEQ ID NO 901  
 LENGTH: 1940  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (0)..(0)  
 OTHER INFORMATION: Polypeptide Accession Number PI1055  
 US-09-538-092-901

Query Match 23.1%; Score 59.5; DB 4; Length 1940;  
 Best local Similarity 35.4%; Pred. No. 40; Mismatches 9; Indels 11; Gaps 3;  
 Matches 17; Conservative 11; Mismatches 9; Indels 11; Gaps 3;

Qy 9 KCQRQIEMNELLNEVALQVDRKVA--DRE---KQSVDAAWATVIS 50  
 Db 1558 KILRIOLELNQVKSE----IDRKIAEKDEBDOLKRNLYQRTVTMQS 1600

RESULT 8 US-09-949-016-8888  
 Sequence 8888, Application US/09949016  
 Patent No. 6812339  
 GENERAL INFORMATION:  
 APPLICANT: Venter, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: C1001307  
 CURRENT APPLICATION NUMBER: US/09/949,016  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 6/0241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 6/0237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 6/0231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSeq For Windows Version 4.0  
 SEQ ID NO 8888  
 LENGTH: 1963  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-949-016-8888

Query Match 23.1%; Score 59.5; DB 4; Length 1963;  
 Best local Similarity 35.4%; Pred. No. 41; Mismatches 9; Indels 11; Gaps 3;  
 Matches 17; Conservative 11; Mismatches 9; Indels 11; Gaps 3;

Qy 9 KCQRQIEMNELLNEVALQVDRKVA--DRE---KQSVDAAWATVIS 50  
 Db 1581 KILRIOLELNQVKSE----IDRKIAEKDEBDOLKRNHLRVVBSMQST 1623

RESULT 9 US-09-080-897-2  
 Sequence 2, Application US/09080897  
 Patent No. 598574  
 GENERAL INFORMATION:  
 APPLICANT: King, Mary-Claire  
 APPLICANT: Lynch, Eric D.  
 APPLICANT: Lee, Ming  
 APPLICANT: Morrow, Jan E.  
 APPLICANT: Welch, Piri L.  
 APPLICANT: Leon, Pedro E.  
 TITLE OF INVENTION: Modulators of Actin  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
 STREET: 75 DENISE DRIVE  
 CITY: HILLSBOROUGH  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94010  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: pc-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/080,897  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OSMAN, RICHARD A.  
 REGISTRATION NUMBER: 36,627  
 REFERENCE/DOCKET NUMBER: UW97-001  
 TELEPHONE: (650) 343-4341  
 TELEFAX: (650) 343-4342  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1248 amino acid  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-080-897-2

Query Match 22.5%; Score 58; DB 2; Length 1248;  
 Best local Similarity 34.0%; Pred. No. 37; Mismatches 22; Indels 0; Gaps 0;  
 Matches 16; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

Qy 2 EKERNPVQKCQRQIEMNELLNEVALQVDRKVADEEKQSVDAAWATV 48  
 Db 517 EKQQIATEKQDLEAVSVOLTGEVAKLTKELEDKEMASLMAITV 563

RESULT 10 US-09-323-735-2  
 Sequence 2, Application US/09323735  
 Patent No. 6197932  
 GENERAL INFORMATION:  
 APPLICANT: King, Mary-Claire  
 APPLICANT: Lynch, Eric D.  
 APPLICANT: Lee, Ming  
 APPLICANT: Morrow, Jan E.  
 APPLICANT: Welch, Piri L.  
 APPLICANT: Leon, Pedro E.  
 TITLE OF INVENTION: Modulators of Actin  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
 STREET: 75 DENISE DRIVE  
 CITY: HILLSBOROUGH  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94010

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/323,735  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 09/080,897

ATTORNEY/AGENT INFORMATION:  
 NAME: OSMAN, RICHARD A  
 REFERENCE/DOCKET NUMBER: 36,627

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 343-4342  
 TELEFAX: (650) 343-4342  
 MOLECULE TYPE: Peptide  
 US-09-323-735-2

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1249 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

Query Match 22.5%; Score 58; DB 3; Length 1248;  
 Best Local Similarity 34.0%; Pred. No. 37; Matches 16; Conservative 9; Mismatches 22; Indels 0; Gaps 0;  
 QY 2 EKETPVQKCORLQIEMNELLNEVALQVDRKVADEEKQSVDVVATV 48  
 Db 517 EKQQITAQOKDDEAIVSQLGEVAKLTKELEDAKKNEMASLSAAITV 563

RESULT 11  
 US-09-080-897-4  
 Sequence 4, Application US/09080897  
 Patent No. 5985574

GENERAL INFORMATION:  
 APPLICANT: KING, Mary-Claire  
 APPLICANT: Lynch, Eric D.  
 APPLICANT: Lee, Ming  
 APPLICANT: Morrow, Jan E.  
 APPLICANT: Welch, Piri L.  
 APPLICANT: Leon, Pedro E.  
 TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN M6A AND GENE

Query Match 22.5%; Score 58; DB 2; Length 1255;  
 Best Local Similarity 35.8%; Pred. No. 37; Matches 19; Conservative 10; Mismatches 22; Indels 2; Gaps 1;  
 QY 2 EKETPVQKCORLQIEMNELLNEVALQVDRKVADEEKQSVDVVATV 52  
 Db 517 EKQQITAQOKDDEAIVSQLGEVAKLTKELEDAKKNEMASLSAAITV 569

RESULT 12  
 US-08-899-595-1  
 Sequence 1, Application US/08899595  
 Patent No. 611072

GENERAL INFORMATION:  
 APPLICANT: Narumiya, Shuh  
 APPLICANT: Takahashi, No. 611072uaki  
 TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN M6A AND GENE

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20007-5109

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/899,595  
 FILING DATE: 24-JUL-1997  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 8-242701  
 FILING DATE: 26-AUG-1996

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 9-90170  
 FILING DATE: 25-MAR-1997

ATTORNEY/AGENT INFORMATION:  
 NAME: Stephen A. Bent  
 REGISTRATION NUMBER: 29,768  
 REFERENCE/DOCKET NUMBER: 049441/0112

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 672-5300  
 TELEFAX: (202) 672-5399  
 TELEX: 904136

INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1255 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-899-595-1

Query Match 22.5%; Score 58; DB 3; Length 1255;  
 Best Local Similarity 35.8%; Pred. No. 37;

ATTORNEY/AGENT INFORMATION:  
 NAME: OSMAN, RICHARD A

Matches 19; Conservative 10; Mismatches 22; Indels 2; Gaps 1;

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/899,595

FILING DATE: 24-JUL-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 8-242701

FILING DATE: 26-AUG-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 9-90170

FILING DATE: 25-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Stephen A. Bent

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 049441/0112

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEX: 904136

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1315 amino acids

TYPE: amino acid

TOPOLOGY: Linear

MOLECULE TYPE: protein

US-08-899-595-3

Query Match 22.5%; Score 58; DB 3; Length 1255;

Best Local Similarity 34.0%; Pred. No. 39; Mismatches 22; Indels 0; Gaps 0;

Matches 16; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

Sequence 23:627, Application US/09252991A

PATENT NO. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196-136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,798

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 23:627

LENGTH: 1413

TYPE: RPT

ORGANISM: Pseudomonas aeruginosa

US-09-232-991A-23627

Query Match 22.5%; Score 58; DB 4; Length 1413;

Best Local Similarity 31.5%; Pred. No. 43; Mismatches 16; Indels 10; Gaps 2;

Matches 17; Conservative 11; Mismatches

APPLICANT: Narumiya, Shuh

APPLICANT: Takahashi, No. 6111072uaki

TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDA AND GENE

TITLE OF INVENTION: ENCODING SAME

RESULT 14

US-08-899-595-3

Sequence 3, Application US/08899595

PATENT NO. 6111072

GENERAL INFORMATION:

APPLICANT: Narumiya, Shuh

APPLICANT: Takahashi, No. 6111072uaki

TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDA AND GENE

TITLE OF INVENTION: ENCODING SAME

RESULT 13

US-09-323-735-4

Sequence 4, Application US/09323735

PATENT NO. 6119792

GENERAL INFORMATION:

APPLICANT: King, Mary-Claire

APPLICANT: Lynch, Eric D.

APPLICANT: Lee, Ming

APPLICANT: Morrow, Jan E.

APPLICANT: Welch, Piri L.

APPLICANT: Leon, Pedro B.

TITLE OF INVENTION: Modulators of Actin

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 75 DENISE DRIVE

CITY: HILLSBOROUGH

STATE: CALIFORNIA

ZIP: 94010

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/323,735

FILING DATE: 24-JUL-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 9-90170

FILING DATE: 25-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Stephen A. Bent

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 049441/0112

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEX: 904136

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1315 amino acids

TYPE: amino acid

TOPOLOGY: Linear

MOLECULE TYPE: protein

US-09-323-735-4

Query Match 22.5%; Score 58; DB 3; Length 1255;

Best Local Similarity 34.0%; Pred. No. 37; Mismatches 22; Indels 2; Gaps 1;

Matches 19; Conservative 10; Mismatches 22; Indels 2; Gaps 1;

Sequence 2:627, Application US/09252991A

PATENT NO. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196-136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,798

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 23:627

LENGTH: 1413

TYPE: RPT

ORGANISM: Pseudomonas aeruginosa

Mon Nov 7 09:42:39 2005

09782816-52.ra1

Page 6

Qy 6 PVQKCOR--LQTEKNNELNEVAALQVDREKVAD-----EJKOSYDAYVATVI 49  
|:||| |:| :| |:| |:| |:| |:| |:| |:| |:|  
Db 857 PAQRCQRGVLGVQRRAVLLAPARHACROLAEGLERORVVAEOQAYAAVLDHVL 910

Search completed: November 3, 2005, 22:05:58  
Job time : 28.2086 secs

GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: November 3, 2005, 21:53:15 ; Search time 95.5134 Seconds

(without alignment) 232.174 Million cell updates/sec

Title: 09782816-52

Perfect score: 258

Sequence: 1 GEKETPVQKCORLQIENNEL...ADEEKQSYDAVATVISTAR 53

Scoring table: BL0SUM62

Gappen 10.0 , Gapext: 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters:

1867879

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_R4: \*

1: /cgpn2\_6/ptodata/1/pubpaas/US07\_PUBCOMB.pep: \*

2: /cgpn2\_6/ptodata/1/pubpaas/PCT\_NEW\_PUB.pep: \*

3: /cgpn2\_6/ptodata/1/pubpaas/US06\_NEW\_PUB.pep: \*

4: /cgpn2\_6/ptodata/1/pubpaas/US07\_PUBCOMB.pep: \*

5: /cgpn2\_6/ptodata/1/pubpaas/US07\_NEW\_PUB.pep: \*

6: /cgpn2\_6/ptodata/1/pubpaas/PCOMB\_PUBCOMB.pep: \*

7: /cgpn2\_6/ptodata/1/pubpaas/US08\_PUBCOMB.pep: \*

8: /cgpn2\_6/ptodata/1/pubpaas/US09\_PUBCOMB.pep: \*

9: /cgpn2\_6/ptodata/1/pubpaas/US09C\_PUBCOMB.pep: \*

10: /cgpn2\_6/ptodata/1/pubpaas/US09\_NNEW\_PUB.pep: \*

11: /cgpn2\_6/ptodata/1/pubpaas/US09\_PUBCOMB.pep: \*

12: /cgpn2\_6/ptodata/1/pubpaas/US10\_PUBCOMB.pep: \*

13: /cgpn2\_6/ptodata/1/pubpaas/US10\_PUBCOMB.pep: \*

14: /cgpn2\_6/ptodata/1/pubpaas/US10B\_PUBCOMB.pep: \*

15: /cgpn2\_6/ptodata/1/pubpaas/US10C\_PUBCOMB.pep: \*

16: /cgpn2\_6/ptodata/1/pubpaas/US10D\_PUBCOMB.pep: \*

17: /cgpn2\_6/ptodata/1/pubpaas/US10E\_PUBCOMB.pep: \*

18: /cgpn2\_6/ptodata/1/pubpaas/US10F\_PUBCOMB.pep: \*

19: /cgpn2\_6/ptodata/1/pubpaas/US11A\_PUBCOMB.pep: \*

20: /cgpn2\_6/ptodata/1/pubpaas/US11\_NEW\_PUB.pep: \*

21: /cgpn2\_6/ptodata/1/pubpaas/USGO\_NEW\_PUB.pep: \*

22: /cgpn2\_6/ptodata/1/pubpaas/USGO\_PUBCOMB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score % Query Match Length DB ID Description

1 258 100.0 53 10 US-09-782-816A-52 Sequence 52, Appl

2 243.5 94.4 380 10 US-09-782-816A-56 Sequence 56, Appl

3 243.5 94.4 380 20 US-11-097143-4056 Sequence 4056, Appl

4 114.2 22 10 US-09-782-816A-26 Sequence 26, Appl

5 108 41.9 21 10 US-09-782-816A-27 Sequence 27, Appl

6 105 40.7 22 10 US-09-782-816A-2 Sequence 2, Appl

7 103 39.9 20 10 US-09-782-816A-28 Sequence 28, Appl

8 98 38.0 19 10 US-09-782-816A-29 Sequence 29, Appl

9 93 36.0 18 10 US-09-782-816A-30 Sequence 30, Appl

10 88 34.1 17 10 US-09-782-816A-31 Sequence 31, Appl

11 81 31.4 16 10 US-09-782-816A-32 Sequence 32, Appl

## ALIGNMENTS

## RESULT 1

US-09-782-816A-52

Sequence 52, Application US/09782816A

Publication No. US20030032771A1

## GENERAL INFORMATION:

APPLICANT: Sharp, David J.

APPLICANT: Rogers, Gregory C.

APPLICANT: Scholey, Jonathan M.

TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR

FILE REFERENCE: U069\_001A

CURRENT APPLICATION NUMBER: US/09/782,816A

CURRENT FILING DATE: 2001-02-14

NUMBER OF SEQ ID NOS.: 56

SOFTWARE: FastSISQ for Windows Version 4.0

SEQ ID NO: 52

LENGTH: 53

TYPE: PRT

ORGANISM: Drosophila melanogaster

Query Match Best Local Similarity 100.0%; Score 258; DB 10; Length 53;

Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ov Db 1 GEKETPVQKCORLQIENNELNEVALQDRKVADEEKQSYDAVATVISTAR 53

1 GEKETPVQKCORLQIENNELNEVALQDRKVADEEKQSYDAVATVISTAR 53

RESULT 2

; Sequence 56, Application US/09782816A

; Publication No. US20030032771A1

```

GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
FILE REFERENCE: UC069_001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 56
LENGTH: 380
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-782-816A-56

RESULT 3
Query Match 94.4%; Score 243.5; DB 10; Length 380;
Best Local Similarity 98.1%; Pred. No. 1.6e-22; Mismatches 0; Indels 1; Gaps 1;
Matches 52; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 GEKETPVOKCQLQIEMNELLNEVALQYDRKVADEEKOSYDAVATVISTAR 53
Db 94 GEKETPVOKCQLQIEMNELLNEVALQYDRKVADEEKOSYDA-VATVISTAR 145

US-11-097-143-4056
Sequence 4056, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID EXPRESSION KITS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DIROSPHILA GENES.
FILE REFERENCE: CL007278
CURRENT APPLICATION NUMBER: US/11/097,143
PRIORITY FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 4056
LENGTH: 380
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-11-097-143-4056

RESULT 4
Query Match 94.4%; Score 243.5; DB 20; Length 380;
Best Local Similarity 98.1%; Pred. No. 1.6e-22; Mismatches 0; Indels 1; Gaps 1;
Matches 52; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 GEKETPVOKCQLQIEMNELLNEVALQYDRKVADEEKOSYDAVATVISTAR 53
Db 94 GEKETPVOKCQLQIEMNELLNEVALQYDRKVADEEKOSYDA-VATVISTAR 145

US-09-782-816A-26
Sequence 26, Application US/09/782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
FILE REFERENCE: UC069_001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 26
LENGTH: 22
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-782-816A-26

RESULT 5
Query Match 44.2%; Score 114; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e-07; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GEKETPVOKCQLQIEMNELLIN 22
Db 1 GEKETPVOKCQLQIEMNELLIN 22

US-09-782-816A-27
Sequence 27, Application US/09/782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
FILE REFERENCE: UC069_001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 27
LENGTH: 21
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-782-816A-27

RESULT 6
Query Match 41.9%; Score 108; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e-07; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 EKETPVOKCQLQIEMNLLIN 22
Db 1 EKETPVOKCQLQIEMNLLIN 21

US-09-782-816A-2
Sequence 2, Application US/09/782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
FILE REFERENCE: UC069_001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56

```

```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ_ID NO 2
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-782-816A-2

Query Match 40.7%; Score 105; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 EVALQVBRKVABEKQSYDAV 44
Db 1 EVALQVDRKVADBEKQSYDAV 22

RESULT 7
US-09-782-816A-28
Sequence 28, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.

APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: UC069..001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ_ID NO 28
LENGTH: 20
TYPE: PRT
ORGANISM: Drosophila melanogaster

RESULT 8
US-09-782-816A-28
Query Match 39.9%; Score 103; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KEPVVKCQLQIEMNELLN 22
Db 1 KEPVVKCQLQIEMNELLN 20

RESULT 9
US-09-782-816A-30
Sequence 30, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: UC069..001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ_ID NO 30
LENGTH: 18
TYPE: PRT
ORGANISM: Drosophila melanogaster

RESULT 10
US-09-782-816A-31
Sequence 31, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: UC069..001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ_ID NO 31
LENGTH: 17
TYPE: PRT
ORGANISM: Drosophila melanogaster

RESULT 11
US-09-782-816A-32
Sequence 32, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION

```

Query Match 38.0%; Score 98; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-05; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ETPVKCQLQIEMNELLN 22
Db 1 PVVKCQLQIEMNELLN 17

```

; FILE REFERENCE: UC069_001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-782-816A-32

Query Match 31.4%; Score 81; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0019; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 VOKCQLQIEMNELLN 22
Db 1 VOKCQLQIEMNELLN 16

RESULT 12
US-09-782-816A-33
; Sequence 33, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathon M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR PROLIFERATION
; FILE REFERENCE: UC069_001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ For Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-782-816A-33

Query Match 29.8%; Score 77; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0058; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 QKCORLIQIEMNELLN 22
Db 1 QKCORLIQIEMNELLN 15

RESULT 13
US-09-782-816A-54
; Sequence 54, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathon M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR PROLIFERATION
; FILE REFERENCE: UC069_001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE: NAME/KEY: UNSURE
; LOCATION: 44
; OTHER INFORMATION: Xaa = Val or Ieu
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus musculus.
; OTHER INFORMATION: musculus.
; SEQ ID NO 54
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-782-816A-54

Query Match 28.7%; Score 74; DB 10; Length 183;
Best Local Similarity 35.8%; Pred. No. 0.32; Mismatches 14; Indels 1; Gaps 1;
Qy 1 GEKETPVOKCQLQIEMNELLNNEVALQD-RKVADEEK 38
Db 1 GVKETPQOKYQRLHLHEVQBLTTEVEKIKITVKESATEK 39

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Mon Nov 7 09:42:39 2005

09782816-52.rapb

Page 5

Search completed: November 3, 2005, 22:11:41  
Job time : 96.5134 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:43:09 ; Search time 18.9091 Seconds  
 (without alignments)  
 264.596 Million cell updates/sec

Title: 09782816-51  
 Perfect score: 251  
 Sequence: 1 GVKETPQQKVQLLHEWQEL.....ESATEEKITPVLLAKQAL 52  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext: 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database : PIR\_70;\*

1: pix1;\*  
 2: pix2;\*  
 3: pix3;\*  
 4: pix4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	% Query Match	Length	DB ID	Description
1	69.5	27.7	804	T32864	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
2	68	27.1	1742	T49451	hypothetical protein
3	67.5	26.9	1325	2 S16129	kinesin-like prote
4	67	26.7	1287	T2235	dynamin-associated
5	67	26.7	2481	D90011	hypothetical prote
6	66	26.3	393	2 T04957	FmTB protein
7	66	26.3	866	2 C71509	hypothetical prote
8	65.5	26.1	1837	T41023	probable DNA polym
9	64	25.5	210	2 E84499	probable nuclear p
10	63.5	25.3	163	S69518	hypothetical prote
11	63	25.1	374	D70391	hypothetical prote
12	63	25.1	281	2 F75216	hypothetical prote
13	63	25.1	314	2 F90577	lipoprotein vba
14	62.5	24.9	1281	2 JC5368	l
15	62	24.7	296	2 T32222	dynactin 1 - mouse
16	62	24.7	2469	H38612	hypothetical prote
17	61	24.3	442	2 C95070	senior histidine k
18	61	24.3	442	2 A97938	vncS - histidine ki
19	60.5	24.1	1214	2 JC2029	hypothetical prote
20	60.5	24.1	523	2 S06920	zinc-finger protei
21	60	23.9	695	2 H72243	glucose transport
22	60	23.9	695	D71453	translation elonga
23	59.5	23.7	665	2 S62328	hypothetical prote
24	59.5	23.7	665	2 G72645	kinesin-like DNA b
25	59	23.5	112	2 D84004	hypothetical prote
26	59	23.5	239	G85436	hypothetical prote
27	59	23.5	550	2 E90543	hypothetical prote
28	59	23.5	611	2 A34219	glucose inhibited
29	59	23.5	782		Bic-D protein - fr

**ALIGNMENTS**

RESULT 1

Query Match 27.7; Score 69.5; DB 2; Length 804;  
 Best Local Similarity 34.4%; Pred. No. 20; Mismatches 19; Indels 13; Gaps 3;

Matches 22; Conservative 10; Mismatches 19; Indels 13; Gaps 3;

QY 2 VKEFPPQQKVQLLHEWQEL-----KIKT-TVKSATEE-KLTVLLAKQ 48

Db 366 VEDPDPDEKKVQKTTKVEIEMNEEEDGEIGAESTSKRKVTKBIDEEVKQTEMKLA 425

OY 49 LAAL 52

DB 426 SKL 429

RESULT 2

Query Match 27.7; Score 69.5; DB 2; Length 804;  
 Best Local Similarity 34.4%; Pred. No. 20; Mismatches 19; Indels 13; Gaps 3;

Matches 22; Conservative 10; Mismatches 19; Indels 13; Gaps 3;

QY 2 VKEFPPQQKVQLLHEWQEL-----KIKT-TVKSATEE-KLTVLLAKQ 48

Db 366 VEDPDPDEKKVQKTTKVEIEMNEEEDGEIGAESTSKRKVTKBIDEEVKQTEMKLA 425

OY 49 LAAL 52

DB 426 SKL 429

Q;Alternate names: Protein Bl4D6\_30  
 N;Species: *Neurospora crassa*  
 C;Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
 C;Accession: T49451  
 R;Schulze, U.; Aigr, V.; Hoheisel, J.; Brandt, P.; Fertmann, B.; Holland, R.; Nyakatura, A.;Reference number: Z25022  
 A;Accession: T49451  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-1742 <SCH>  
 A;Cross-references: UNIPROT:Q8X0C5; EMBL:AU356173; GSPDB:GN00116; NCSP:Bl4D6\_30  
 C;Genetics:



Best local Similarity 36.4%; Pred. No. 50; Matches 20; Conservative 10; Mismatches 21; Indels 4; Gaps 2;

Qy 1 GVKETPQQKTYQLRMB--VQELTTEVEKIKTVKESATEBKLTPTVLAKQAL 52  
Db 188 GVGCGCPKKAQKLLERFQSVEELVANTERLSGKTKOMIEDQKET-LILSKRQATL 241

**RESULT 8**

T41023 probable nuclear pore complex-associated protein - fission yeast (*Schizosaccharomyces pombe*)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T41023  
R;Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, June 1998

A;Reference number: Z21965  
A;Accession: T41023  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-163 <ESP>  
A;Cross-references: UNIPROT:P51714; EMBL:U24159; NID:91046235; PIDN:AB09197.1; PID:9104  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995  
C;Superfamily: phage HPI hypothetical protein 12

Query Match 25.3%; Score 63.5; DB 2; Length 163;  
Best Local Similarity 37.8%; Pred. No. 15; Mismatches 17; Conservative 11; Indels 1; Gaps 1;

Matches 19; Conservative 10; Mismatches 17; Indels 7; Gaps 2;

Qy 7 QKQYQRLHVEQELTTEVEKIKTV--KESATEBKLTPTVLAK---QLAQ 52  
Db 662 QTSYQSRSLTRLEQTLNELESIISRNKEKKFERAIISSQLEKSNIQLOQTL 714

**RESULT 9**

EB4499 hypothetical protein At2g11890 [imported] - *Arabidopsis thaliana*  
C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Accession: EB4499  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 12-Jul-2004  
C;Accession: EB4499  
R;Jin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayan, L.; Talton, L.;  
Euseb, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A;Reference number: A84420; PMID:20083487; PMID:10617197  
A;Accession: EB4499  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-210 <STO>  
A;Cross-references: UNIPROT:Q9SIY3; GB:AE002093; NID:94557062; PIDN:AAD22501.1; GSDB:GN  
C;Genetics:  
A;Gene: At2g11890  
A;Map position: 2  
C;Superfamily: uncharacterized CYTH domain protein

Query Match 25.5%; Score 64; DB 2; Length 210;  
Best Local Similarity 40.5%; Pred. No. 17; Mismatches 17; Conservative 9; Indels 14; Indels 2; Gaps 2;

Qy 1 GVKETPQQKTYQLRMB--VQELTTEVEKIKTVKESATEBKLTPTVLAKQAL 51  
Db 150 GVKETPQQKTYQLRMB--VQELTTEVEKIKTVKESATEBKLTPTVLAKQAL 191

**RESULT 10**

S69518 hypothetical protein 12 - phage HPI  
C;Species: phage HPI  
C;Accession: 06-Dec-1995 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S69518

R;Esposito, D.; Fitzmaurice, W.P.; Benjamin, R.C.; Goodman, S.D.; Waldman, A.S.; Scocca,  
Nucleic Acids Res. 24, 2360-2368, 1996  
A;Title: The complete nucleotide sequence of bacteriophage HPI DNA.  
A;Reference number: S69503; MUID:96279738; PMID:8710508  
A;Accession: S69518  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-163 <ESP>  
A;Cross-references: UNIPROT:P51714; EMBL:U24159; NID:91046235; PIDN:AB09197.1; PID:9104  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995  
C;Superfamily: phage HPI hypothetical protein 12

Query Match 25.3%; Score 63.5; DB 2; Length 163;  
Best Local Similarity 37.8%; Pred. No. 15; Mismatches 17; Conservative 11; Indels 1; Gaps 1;

Matches 19; Conservative 10; Mismatches 17; Indels 7; Gaps 2;

Qy 5 TPQKQYQRLHVEQELTTEVEKIK-TVKESATEBKLTPTVLAKQ 48  
Db 25 TPQKQYQRLHVEQELTTEVEKIK-TVKESATEBKLTPTVLAKQ 69

**RESULT 11**

D70391 hypothetical protein aq\_1060 - *Aquifex aeolicus*  
C;Species: Aquifex aeolicus  
C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C;Accession: D70391  
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov  
V.; Nature 332, 353-358, 1998  
A;Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.  
A;Reference number: A70300; MUID:9819666; PMID:9537320  
A;Accession: D70391  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-374 <AQF>  
A;Cross-references: UNIPROT:O67159; GB:AE000721; NID:92983544; PIDN: AAC07129.1; PID:929  
A;Experimental source: strain VF5  
C;Genetics:  
A;Gene: aq\_1060  
C;Superfamily: multidrug resistance protein A; lipoyl/biotin-binding homology  
C;Accession: EB4499  
R;Jin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayan, L.; Talton, L.;  
Euseb, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A;Reference number: A84420; PMID:20083487; PMID:10617197  
A;Accession: EB4499  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-210 <STO>  
C;Genetics:  
A;Gene: At2g11890  
A;Map position: 2  
C;Superfamily: uncharacterized CYTH domain protein

Query Match 25.3%; Score 63.5; DB 2; Length 214;  
Best Local Similarity 31.1%; Pred. No. 36; Mismatches 19; Conservative 14; Indels 13; Indels 15; Gaps 3;

Matches 19; Conservative 14; Mismatches 13; Indels 15; Gaps 3;

Qy 6 PQQKQQR-----LHE-----VQELTTEVEKIKTVKESATEBKLTPTVLAKQAL 51  
Db 164 PRRKEEEVDNLKVILHREYLEKSIQEINTEIKRAKGKI-ENARNEFKTIEELKKELS 222

Qy 52 L 52  
Db 223 L 223

**RESULT 12**

F75216 hypothetical protein PHB2181 - *Pyrococcus abyssi* (strain Orsay)  
C;Species: Pyrococcus abyssi  
C;Accession: F75216  
R;anonymous' Genoscope  
C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C;Accession: F75216  
R;anonymous' Genoscope  
C;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru  
A;Reference number: A75001  
A;Accession: F75216  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-221 <KAW>  
A;Cross-references: UNIPROT:Q9V217; GB:AJ248283; GB:AL096836; NID:95457433; PIDN: CAB4918  
A;Experimental source: strain Orsay  
C;Genetics:  
A;Gene: PAB2181

Query Match 25.1%; Score 63; DB 2; Length 281;  
 Best Local Similarity 36.6%; Pred. No. 30;  
 Matches 15; Conservative 12; Mismatches 12; Indels 2; Gaps 2;

Qy 1 GVKE-TPOOKYQRLHVOELTTEVEKIKITVKESATEEKLTIVLAKQL 40  
 Db 119 GIKEVVAAREEYEKLIKKEYERKLQEFPEEVKAKI-EAELESL 158

RESULT 13  
 F90577  
 lipoprotein vsaE [Imported] - Mycoplasma pulmonis (strain UAB CTIP) (fragment)  
 C;Species: Mycoplasma pulmonis  
 C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
 C;Accession: F90577  
 R;Chambard, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;  
 Nucleic Acids Res. 29, 2145-2153, 2001.  
 A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm  
 A;Reference number: A99512; MUID:21267165; PMID:11353084  
 A;Accession: F90577  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-22 <DAV>  
 A;Cross-references: UNIPROT:Q98Q43; GB:AL445566; PID:914089940; PIDN:CAC13699.1; GSPPDB:G  
 A;Experimental source: strain UAB CTIP  
 A;Experimental source: strain Bristol N2; clone T23B12  
 C;Genetics:  
 A;Gene: MYPU\_5260  
 A;Genetic code: SGC3

Query Match 25.1%; Score 63; DB 2; Length 314;  
 Best Local Similarity 29.8%; Pred. No. 34;  
 Matches 14; Conservative 17; Mismatches 10; Indels 6; Gaps 2;

Qy 2 WKETPQQKYQRLHVOELTTEVEKIKITVKESATEEKLTIVLAKQL 44  
 Db 246 ITEEQKAKPKIVIQDARTKLUQDLTTKLEKIKSS--EKENIEKKLDPII 290

RESULT 14  
 JC5368  
 dynatin 1 - mouse  
 N;Alternate names: p150 Glued  
 C;Species: Mus musculus (house mouse)  
 C;Date: 28-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 09-Jul-2004  
 C;Accession: JC5368  
 R;Jang, W.; Weber, J.S.; Tokito, M.K.; Holzbaier, E.L.F.; Meissler, M.H.  
 Bloch, M. Biophys. Res. Commun. 231, 344-347, 1997  
 A;Title: Mouse p150Glued (dynactin 1) cDNA sequence and evaluation as a candidate for th  
 A;Reference number: JC5368; MUID:97223454; PMID:9070275  
 A;Accession: JC5368  
 A;Molecule type: mRNA  
 A;Residues: 1-1281 <JAN>  
 A;Cross-references: UNIPROT:Q008788; GB:U60312; NID:g2104494; PIDN:AA857773.1; PID:921044  
 A;Experimental source: brain  
 C;Comment: This protein is a member of the oligomeric dynein complex that is required  
 C;Genetics:  
 A;Gene: Dctnl  
 A;Map position: 6

Query Match 24.9%; Score 62.5; DB 2; Length 1281;  
 Best Local Similarity 34.8%; Pred. No. 1.8e+02;  
 Matches 16; Conservative 11; Mismatches 18; Indels 1; Gaps 1;

Qy 4 ETPOOKYQRLHVOELTTEVEKIKITVKESATEEKLTIVLAKQL 49  
 Db 319 ESLQQEVEALKERVDELTDILEILKAIEEKGSGDGAASVQL-KQL 363

RESULT 15  
 T3222  
 hypothetical protein T23B12.7 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans

Run on: November 3, 2005, 21:51:39 ; Search time 15.4011 Seconds  
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GenCore version 5.1.6

OM protein - protein search, using sw model

Title:	November 3, 2005, 21:51:39 ; Search time 15.4011 Seconds (without alignments) 145.410 Million cell updates/sec									
Perfect score:	09782816-1-22 1 EKEVKKTTVRESATEEKUTPVLLAKQAL 30									
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5									
Searched:	513545 seqs, 74649064 residues									
Total number of hits satisfying chosen parameters:	513545									
Minimum DB seq length:	0									
Maximum DB seq length:	200000000									
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries									
Database :	<b>Issued Patents AA:*</b> 1: /cgn2_6/pctodata/1/iaa/5A_COMB.pep: * 2: /cgn2_6/pctodata/1/iaa/5B_COMB.pep: * 3: /cgn2_6/pctodata/1/iaa/6A_COMB.pep: * 4: /cgn2_6/pctodata/1/iaa/6B_COMB.pep: * 5: /cgn2_6/pctodata/1/iaa/PCTUS COMB.pep: * 6: /cgn2_6/pctodata/1/iaa/backfile1.pep: *									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.										
SUMMARIES										
Result No.	Score	% Match	Query Length	DB ID	Description					
1	51	37.0	136	4	US-09-270-767-36154	Sequence 36154, A				
2	51	37.0	136	4	US-09-270-767-51371	Sequence 51371, A				
3	50	36.2	938	4	US-09-637-145-2	Sequence 2, Appl				
4	49.5	35.9	119	4	US-09-621-976-4332	Sequence 4332, Appl				
5	49	35.5	413	4	US-09-107-532A-433	Sequence 6433, Appl				
6	49	35.5	1027	4	US-09-107-532B-6675	Sequence 6675, Appl				
7	48.5	35.1	124	4	US-09-513-999C-6026	Sequence 6026, Appl				
8	48.5	35.1	280	3	US-09-470-512A-14	Sequence 14, Appl				
9	48.5	35.1	451	4	US-09-767-45139	Sequence 45139, Appl				
10	48	34.8	107	4	US-09-107-532A-6432	Sequence 6432, Appl				
11	48	34.8	1200	4	US-09-634-827B-8	Sequence 8, Appl				
12	48	34.8	1428	4	US-09-634-827B-7	Sequence 7, Appl				
13	47.5	34.4	167	4	US-09-166-350-13	Sequence 13, Appl				
14	47.5	34.4	314	4	US-09-902-540-16180	Sequence 16180, Appl				
15	47.5	34.4	403	4	US-09-976-594-421	Sequence 421, Appl				
16	47	34.1	103	4	US-09-132-210-1198	Sequence 1198, Appl				
17	47	34.1	180	4	US-09-648-004-2	Sequence 2, Appl				
18	47	34.1	180	4	US-10-212-419-2	Sequence 2, Appl				
19	47	34.1	289	4	US-09-071-035-480	Sequence 480, Appl				
20	47	34.1	317	3	US-09-134-001C-3712	Sequence 3712, Appl				
21	47	34.1	387	4	US-09-248-796A-18485	Sequence 18485, Appl				
22	47	34.1	424	4	US-09-286-981B-14	Sequence 14, Appl				
23	47	34.1	425	4	US-09-286-981B-13	Sequence 13, Appl				
24	47	34.1	426	4	US-09-286-981B-12	Sequence 12, Appl				
25	47	34.1	708	4	US-09-071-035-256	Sequence 256, Appl				
26	47	34.1	894	4	US-09-071-035-248	Sequence 248, Appl				
27	47	34.1	894	4	US-09-071-035-248	Sequence 248, Appl				

Query Match Best Local Similarity 37.0%; Score 51; DB 4; Length 136;  
 Matches 14; Conservat. 6; Mismatches 9; Indels 6; Gaps 1;

ALIGNMENTS

QY	2 VEKIKTT----VRESATEEKUTPVLLAKQAL 30
Db	37 IDKVKITTPANKPKTPTSNMNMKLSAVLIAAL 71

RESULT 1  
 US-09-270-767-36154

; Sequence 36154, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270, 767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 36154  
 ; LENGTH: 136  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 ; US-09-270-767-36154

RESULT 2  
 US-09-270-767-51371

; Sequence 51371, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270, 767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 51371  
 ; LENGTH: 136  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 ; US-09-270-767-51371

Query Match Best Local Similarity 37.0%; Score 51; DB 4; Length 136;  
 Matches 14; Conservat. 6; Mismatches 9; Indels 6; Gaps 1;

RESULT 3  
 sequence 2, Application US/09637145  
 Patent No. 6673587  
 GENERAL INFORMATION:  
 APPLICANT: EVANS, RONALD M.  
 APPLICANT: KAO, HUNG-YING  
 APPLICANT: DORNES, MICHAEL  
 APPLICANT: ORENTLICH, PETER  
 TITLE OF INVENTION: NOVEL HISTONE DEACETYLASE, AND USES THEREFOR  
 FILE REFERENCE: SALK300  
 CURRENT APPLICATION NUMBER: US/09/637,145  
 CURRENT FILING DATE: 2000-08-11  
 NUMBER OF SEQ ID NOS: 4  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 2  
 LENGTH: 938  
 TYPE: PRT  
 ORGANISM: Mus sp.

US-09-637-145-2

Query Match 36.2%; Score 50; DB 4; Length 938;  
 Best Local Similarity 44.0%; Pred. No. 94; Mismatches 9; Indels 0; Gaps 0;

QY 6 RTTVKVKESATEBKLTPTVLLAKQAL 30  
 Db 100 RSAYAVSVVVKQKLAIVLKQOAL 124

RESULT 4  
 US-09-621-976-4332  
 Sequence 4332, Application US/09621976  
 Patent No. 6639053  
 GENERAL INFORMATION:  
 APPLICANT: Dumas Milne Edwards, J.B.  
 APPLICANT: Jobert, S.  
 APPLICANT: Giordano, J.Y.  
 TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
 FILE REFERENCE: GENSET\_054PR2  
 CURRENT APPLICATION NUMBER: US/09/621,976  
 NUMBER OF SEQ ID NOS: 19335  
 SOFTWARE: PatentIn.pm  
 SEQ ID NO 4332  
 LENGTH: 119  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: UNSURE  
 LOCATION: 66  
 OTHER INFORMATION: Xaa = \*, Trp  
 US-09-621-976-4332

Query Match 35.9%; Score 49.5; DB 4; Length 119;  
 Best Local Similarity 40.6%; Pred. No. 11; Mismatches 13; Conservative 7; Mismatches 9; Indels 3; Gaps 1;

QY 1 EVEKIKITVKESATEBKLTPTVLLAK--LAA 29  
 Db 62 ELDKKITMKSSVQECVSISSKEDPLA 93

RESULT 5  
 US-09-107-532A-6433  
 Sequence 6433, Application US/09107532A  
 Patent No. 6583275  
 GENERAL INFORMATION:  
 APPLICANT: Lynn A Doucette-Stamm and David Bush  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
 NUMBER OF SEQUENCES: 7310  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
 STREET: 100 Beaver Street  
 CITY: Waltham  
 STATE: Massachusetts  
 ZIP: 02434  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD/ROM ISO9660  
 COMPUTER: PC

RESULT 6  
 US-09-107-532A-6675  
 Sequence 6675, Application US/09107532A  
 Patent No. 6583275  
 GENERAL INFORMATION:  
 APPLICANT: Lynn A Doucette-Stamm and David Bush  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
 NUMBER OF SEQUENCES: 7310  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
 STREET: 100 Beaver Street  
 CITY: Waltham  
 STATE: Massachusetts  
 ZIP: 02434  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD/ROM ISO9660  
 COMPUTER: PC

TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
 NUMBER OF SEQUENCES: 7310  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
 STREET: 100 Beaver Street  
 CITY: Waltham  
 STATE: Massachusetts  
 ZIP: 02434  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD/ROM ISO9660  
 COMPUTER: PC

ATTORNEY/AGENT INFORMATION:  
 NAME: Arinieillo, Pamela Deniske  
 REGISTRATION NUMBER: 40,489  
 REFERENCE/DOCKET NUMBER: GTC-012  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (781)893-5007  
 TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 6433:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 413 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ORIGINAL SOURCE:  
 ORGANISM: Enterococcus faecium

FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (B) LOCATION 1..413  
 SEQUENCE DESCRIPTION: SEQ ID NO: 6433:  
 US-09-107-532A-6433

Query Match 35.5%; Score 49; DB 4; Length 413;  
 Best Local Similarity 44.4%; Pred. No. 51; Mismatches 12; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 1 EVEKIKITVKESATEBKLTPTVLLAK 25  
 Db 64 EIRSQTVELTKENRILPGGVWLTK 90

OPERATING SYSTEM: <Unknown>  
 SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/107,532A  
 FILING DATE: 30-Jun-1998  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 60/085,598  
 FILING DATE: 14 May 1998  
 APPLICATION NUMBER: 60/051571  
 FILING DATE: July 2, 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Rinallo, Pamela Deneke  
 REGISTRATION NUMBER: 40,489  
 REFERENCE/DOCKET NUMBER: GTC-012  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (781)893-5507  
 TELEX/FAX: (781)893-8277  
 INFORMATION FOR SEQ ID NO: 6675:  
 LENGTH: 1027 amino acids  
 SEQUENCE CHARACTERISTICS:  
 TOPOLY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ORIGINAL SOURCE:  
 ORGANISM: Enterococcus faecium  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (B) LOCATION 1..1027  
 SEQUENCE DESCRIPTION: SEQ ID NO: 6675:  
 , US-09-107-532A-6675

RESULT 7

Query Match 35.5%; Score 49; DB 4; Length 1027;  
 Best Local Similarity 44.4%; Pred. No. 1.4e+02; Mismatches 8; Indels 2; Gaps 1;  
 Matches 12; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

QY 1 EVEKIKTTVKESATEEKLTP--VLLAK 25  
 DB 788 EIERSQTAVVELTKENRLTPGGVVLT 814

US-09-513-999C-6026

; Sequence 6026, Application US/09513999C  
 ; Patent No. 6783961  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Ductert, A.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
 ; Patent No. 6783961  
 ; FILE REFERENCE: 59.US2.REG  
 ; CURRENT APPLICATION NUMBER: US/09/513,999C  
 ; CURRENT FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/122,487  
 ; NUMBER OF SEQ ID NOS: 36681  
 ; SOFTWARE: Patent-ppm  
 ; SEQ ID NO 6026  
 ; LENGTH: 124  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: UNSURE  
 ; LOCATION: 46  
 ; OTHER INFORMATION: Xaa=Gln or Arg  
 ; US-09-513-999C-6026

Query Match 35.1%; Score 48.5; DB 4; Length 124;  
 Best Local Similarity 39.3%; Pred. No. 15; Mismatches 11; Conservative 10; Mismatches 6; Indels 1; Gaps 1;

QY 1 EVEKIKTTVKESATE-EKLTPVLLAKQL 27  
 DB 79 EBEKIKRSIKQAAQKNDRITCVLAKEL 106

US-09-107-532A-6432

; Sequence 6432, Application US/09107532A  
 ; Patent No. 658375  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lynn A Doucette-Slaam and David Bush  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
 ; ENTROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
 ; NUMBER OF SEQUENCES: 7310  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSE: GENOME THERAPEUTICS CORPORATION  
 ; STREET: 100 Beaver Street

RESULT 8

DB 40 EBEKIKRSIKQAAQKNDRITCVLAKEM 67

US-09-470-512A-14

; Sequence 14, Application US/09470512A  
 ; Patent No. 637652  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PhageTech, Inc.  
 ; TITLE OF INVENTION: Compositions and methods involving an essential *Staphylococcus Au*  
 ; TITLE OF INVENTION: gene and its encoded protein  
 ; FILE REFERENCE: 21715/1000  
 ; CURRENT APPLICATION NUMBER: US/09/470,512A  
 ; CURRENT FILING DATE: 1999-12-12  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 14  
 ; LENGTH: 280  
 ; TYPE: PRT  
 ; ORGANISM: *Bacillus subtilis*  
 ; US-09-470-512A-14

Query Match 35.1%; Score 48.5; DB 3; Length 280;  
 Best Local Similarity 33.3%; Pred. No. 39; Mismatches 11; Conservative 8; Mismatches 9; Indels 5; Gaps 1;

QY 2 VEKIKTTVKESATRKL----TPVLLAKQAA 29  
 DB 171 VRELKNLSQDQTLEKRNMRTPVIMDDIGA 203

RESULT 9

US-09-270-767-45139

; Sequence 45139, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hamburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 6517  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 45139  
 ; LENGTH: 451  
 ; TYPE: PRT  
 ; ORGANISM: *Drosophila melanogaster*  
 ; FEATURE:  
 ; OTHER INFORMATION: Xaa means any amino acid  
 ; US-09-270-767-45139

Query Match 35.1%; Score 48.5; DB 4; Length 451;  
 Best Local Similarity 33.3%; Pred. No. 67; Mismatches 11; Conservative 11; Mismatches 5; Indels 1; Gaps 1;

QY 1 EVEKIKTTVKESATE-EKLTPVLLAKQL 27  
 DB 79 EBEKIKRSIKQAAQKNDRITCVLAKEL 106

RESULT 10

US-09-107-532A-6432

; Sequence 6432, Application US/09107532A  
 ; Patent No. 658375  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lynn A Doucette-Slaam and David Bush  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
 ; ENTROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
 ; NUMBER OF SEQUENCES: 7310  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSE: GENOME THERAPEUTICS CORPORATION  
 ; STREET: 100 Beaver Street





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## OM protein - protein search, using sw model

Run on: November 3, 2005, 21:53:15 ; Search time 54.0642 Seconds

(without alignments)  
 232.174 Million cell updates/sec

Title: 09782816-1-22

Perfect score: 138

Sequence: 1 EVEKIKTTVKESATEEKLTTPVILAKQAL 30

## Scoring table:

BLOSUM62 Gapop 10.0 , Gapext: 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters:

1867879

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA \*

1: /cgmn\_6/ptodata/1/pubpa/US07\_PUBCOMB.pep:\*

2: /cgmn\_6/ptodata/1/pubpa/PCT\_NEW\_PUB.pep:\*

3: /cgmn\_6/ptodata/1/pubpa/US06\_NEW\_PUB.pep:\*

4: /cgmn\_6/ptodata/1/pubpa/US06\_PUBCOMB.pep:\*

5: /cgmn\_6/ptodata/1/pubpa/US07\_NEW\_PUB.pep:\*

6: /cgmn\_6/ptodata/1/pubpa/PCITUS\_PUBCOMB.pep:\*

7: /cgmn\_6/ptodata/1/pubpa/US08\_PUBCOMB.pep:\*

8: /cgmn\_6/ptodata/1/pubpa/US09\_PUBCOMB.pep:\*

9: /cgmn\_6/ptodata/1/pubpa/US09\_NEW\_PUB.pep:\*

10: /cgmn\_6/ptodata/1/pubpa/US09\_NPPUBCOMB.pep:\*

11: /cgmn\_6/ptodata/1/pubpa/US10\_PUBCOMB.pep:\*

12: /cgmn\_6/ptodata/1/pubpa/US10A\_PUBCOMB.pep:\*

13: /cgmn\_6/ptodata/1/pubpa/US10B\_PUBCOMB.pep:\*

15: /cgmn\_6/ptodata/1/pubpa/US1C\_PUBCOMB.pep:\*

16: /cgmn\_6/ptodata/1/pubpa/US1D\_PUBCOMB.pep:\*

17: /cgmn\_6/ptodata/1/pubpa/US1E\_PUBCOMB.pep:\*

18: /cgmn\_6/ptodata/1/pubpa/US1I\_NPPUB.pep:\*

19: /cgmn\_6/ptodata/1/pubpa/US1A\_PUBCOMB.pep:\*

20: /cgmn\_6/ptodata/1/pubpa/US11\_NEW\_PUB.pep:\*

21: /cgmn\_6/ptodata/1/pubpa/US16\_NEW\_PUB.pep:\*

22: /cgmn\_6/ptodata/1/pubpa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Query Length	Match DB ID	Description
1	138	100.0	134 14 US-10-106-698-6730	Sequence 6730, Ap
2	138	100.0	401 16 US-10-400-7650-1369	Sequence 1369, Ap
3	138	100.0	406 10 US-09-782-8160-53	Sequence 53, Appl
4	100.0	465 9 US-09-925-298-676	Sequence 676, Appl	
5	138	100.0	465 14 US-10-107-806-676	Sequence 676, Appl
6	135	97.8	183 10 US-09-782-8160-54	Sequence 54, Appl
7	135	97.8	224 16 US-10-425-15-315831	Sequence 315831, Appl
8	133	96.4	52 10 US-09-782-8160-51	Sequence 51, Appl
9	103	74.6	23 10 US-09-782-8160-1	Sequence 1, Appl
10	56	334 18 US-10-501-287-4734	Sequence 4734, Ap	
11	51	37.0	US-10-335-977-7239	Sequence 7239, Ap

## ALIGNMENTS

12	51	37.0	773 15 US-10-335-977-7240	Sequence 7240, Ap
13	51	37.0	932 15 US-10-282-122A-47253	Sequence 47253, A
14	51	37.0	10917 17 US-10-732-923-20606	Sequence 20606, A
15	50	36.2	211 15 US-10-425-115-212374	Sequence 212374,
16	50	36.2	640 15 US-10-282-122A-4691	Sequence 4691, A
17	50	36.2	773 9 US-09-815-242-11330	Sequence 11330, A
18	50	36.2	773 15 US-10-282-122A-58722	Sequence 58722, A
19	50	36.2	855 9 US-09-817-913-13	Sequence 13, Appl
20	50	36.2	855 9 US-09-817-538-13	Sequence 13, Appl
21	50	36.2	855 14 US-10-172-094-9	Sequence 9, Appl
22	50	36.2	855 15 US-10-189-818B-4	Sequence 4, Appl
23	50	36.2	855 16 US-10-870-587-13	Sequence 13, Appl
24	50	36.2	902 16 US-10-437-963-105564	Sequence 105564,
25	50	36.2	912 10 US-09-800-187-12	Sequence 12, Appl
26	50	36.2	915 14 US-10-175-559-2	Sequence 2, Appl
27	50	36.2	933 13 US-10-172-1893	Sequence 183, Ap
28	50	36.2	952 15 US-10-310-534-7	Sequence 7, Appl
29	50	36.2	1642 17 US-10-741-600-1176	Sequence 1176, Ap
30	50	36.2	1642 17 US-10-741-600-1178	Sequence 1178, Ap
31	50	36.2	3024 16 US-10-408-765A-1977	Sequence 1977, Ap
32	50	36.2	3396 16 US-10-788-792-170	Sequence 170, Ap
33	50	36.2	3396 17 US-10-741-600-1172	Sequence 1172, Ap
34	50	36.2	3395 17 US-10-741-600-1173	Sequence 1173, Ap
35	50	36.2	3396 18 US-10-631-467-773	Sequence 773, Ap
36	49	35.5	879 9 US-09-864-761-43703	Sequence 43703, A
37	49	35.5	279 15 US-10-282-122A-57857	Sequence 57857, A
38	49	35.5	291 16 US-10-767-701-40287	Sequence 40287, A
39	49	35.5	307 11 US-09-972-211-73	Sequence 73, Appl
40	49	35.5	307 15 US-10-096-625-73	Sequence 73, Appl
41	49	35.5	340 11 US-09-977-211-72	Sequence 72, Appl
42	49	35.5	49 15 US-09-625-72	Sequence 72, Appl
43	49	35.5	340 16 US-10-723-860-1910	Sequence 1930, Ap
44	49	35.5	340 18 US-10-736-149-520203	Sequence 520203, Ap
45	49	35.5	352 18 US-10-450-763-52703	Sequence 52703, Ap

PRIOR APPLICATION NUMBER: US/10/106,698	CURRENT APPLICATION NUMBER: US/10/106,698	PRIOR FILING DATE: 2002-03-27	PRIOR APPLICATION NUMBER: PCT/US00/26524	PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/10/157,137	PRIOR APPLICATION NUMBER: US/10/157,137	PRIOR FILING DATE: 1999-09-29	PRIOR APPLICATION NUMBER: US/10/163,280	PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 854				
SOFTWARE: PatentIn Ver. 3.0				
SEQ ID NO: 6730				
LENGTH: 134				
TYPE: PRT				
ORGANISM: Homo sapiens				
FEATURE: MISC FEATURE				
NAME/KEY: MISC FEATURE				
LOCATION: (126)				
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids	OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids	OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids	OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids	OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6730	US-10-106-698-6730	US-10-106-698-6730	US-10-106-698-6730	US-10-106-698-6730
Query Match 100.0%; Score 138; DB 14; Length 134;	Query Match 100.0%; Score 138; DB 14; Length 134;	Query Match 100.0%; Score 138; DB 14; Length 134;	Query Match 100.0%; Score 138; DB 14; Length 134;	Query Match 100.0%; Score 138; DB 14; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.3e-11; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity 100.0%; Pred. No. 2.3e-11; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity 100.0%; Pred. No. 2.3e-11; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity 100.0%; Pred. No. 2.3e-11; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity 100.0%; Pred. No. 2.3e-11; Mismatches 0; Indels 0; Gaps 0;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Sequence 1, Appl				
Sequence 2, Appl				
Sequence 3, Appl				
Sequence 4, Appl				
Sequence 5, Appl				
Sequence 6, Appl				
Sequence 7, Appl				
Sequence 8, Appl				
Sequence 9, Appl				
Sequence 10, Appl				
Sequence 11, Appl				
Sequence 12, Appl				
Sequence 13, Appl				
Sequence 14, Appl				
Sequence 15, Appl				
Sequence 16, Appl				
Sequence 17, Appl				
Sequence 18, Appl				
Sequence 19, Appl				
Sequence 20, Appl				
Sequence 21, Appl				
Sequence 22, Appl				

Db 19 EVEKIKTTVKESEATEEKLTIPVLLAKQAL 48  
 RESULT 2  
 US-10-408-765A-1369  
 ; Sequence 1369, Application US/10408765A  
 Publication No. US20040101874A1  
 GENERAL INFORMATION:  
 APPLICANT: Ghosh, Soumitra S.  
 APPLICANT: Fahy, Boin D.  
 APPLICANT: Zhang, Bing  
 APPLICANT: Gibson, Bradford W.  
 APPLICANT: Taylor, Steven W.  
 APPLICANT: Glein, Gary M.  
 APPLICANT: Warnock, Dale E.  
 TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
 TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
 FILE REFERENCE: 660088-465  
 CURRENT APPLICATION NUMBER: US/10/408,765A  
 CURRENT FILING DATE: 2003-04-04  
 NUMBER OF SEQ ID NOS: 3077  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 1369  
 LENGTH: 401  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 ; US-10-408-765A-1369  
 Query Match 100.0%; Score 138; DB 16; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-11;  
 Matches 30; Conservative 0; Mismatches 0;  
 QY 1 EVEKIKTTVKESEATEEKLTIPVLLAKQAL 30  
 Db 116 EVEKIKTTVKESEATEEKLTIPVLLAKQAL 145  
 RESULT 3  
 US-09-782-816A-53  
 ; Sequence 53, Application US/09782816A  
 ; Publication No. US20030032771A1  
 ; GENERAL INFORMATION:  
 APPLICANT: Sharp, David J.  
 APPLICANT: Rogers, Gregory C.  
 APPLICANT: Scholey, Jonathon M.  
 TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR  
 TITLE OF INVENTION: PROLIFERATION  
 FILE REFERENCE: UC009\_001A  
 CURRENT APPLICATION NUMBER: US/09/782,816A  
 CURRENT FILING DATE: 2001-02-14  
 NUMBER OF SEQ ID NOS: 56  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 53  
 LENGTH: 406  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 ; US-09-782-816A-53  
 Query Match 100.0%; Score 138; DB 10; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 8.5e-11;  
 Matches 30; Conservative 0; Mismatches 0;  
 QY 1 EVEKIKTTVKESEATEEKLTIPVLLAKQAL 30  
 Db 121 EVEKIKTTVKESEATEEKLTIPVLLAKQAL 150  
 RESULT 4  
 US-09-925-298-676  
 ; Sequence 676, Application US/09925298  
 Publication No. US20020039764A1  
 GENERAL INFORMATION:  
 APPLICANT: Rosen et al.  
 FEATURE: EAA equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (5)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (6)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (16)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; US-10-102-805-676  
 Query Match 100.0%; Score 138; DB 9; Length 465;  
 Best Local Similarity 100.0%; Pred. No. 1e-10;  
 Matches 30; Conservative 0; Mismatches 0;  
 QY 1 EVEKIKTTVKESEATEEKLTIPVLLAKQAL 30  
 Db 180 EVEKIKTTVKESEATEEKLTIPVLLAKQAL 209  
 RESULT 5  
 US-10-102-805-676  
 ; Sequence 676, Application US/10102806  
 ; Publication No. US20030054421A1  
 ; GENERAL INFORMATION:  
 APPLICANT: Roben et al.  
 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 FILE REFERENCE: PAI03P1C1  
 CURRENT APPLICATION NUMBER: US/10/102,806  
 CURRENT FILING DATE: 2002-03-22  
 PRIOR APPLICATION NUMBER: 09/925,298  
 PRIOR FILING DATE: 2001-08-10  
 PRIOR APPLICATION NUMBER: PCT/US00/05881  
 PRIOR FILING DATE: 2000-03-08  
 PRIOR APPLICATION NUMBER: 60/124,270  
 PRIOR FILING DATE: 1999-03-12  
 NUMBER OF SEQ ID NOS: 845  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 676  
 LENGTH: 465  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE: EAA equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (5)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (6)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (16)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; US-10-102-805-676  
 Query Match 100.0%; Score 138; DB 14; Length 465;  
 Best Local Similarity 100.0%; Pred. No. 1e-10;  
 Matches 30; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

RESULT 6  
 US-09-782-816A-54  
 ; Sequence 54, Application US/09782816A  
 ; Publication No. US20030032771A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sharp, David J.  
 ; APPLICANT: Rogers, Gregory C.  
 ; APPLICANT: Scholey, Jonathon M.  
 ; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR PROLIFERATION  
 ; TITLE OF INVENTION: PROLIFERATION  
 ; CURRENT APPLICATION NUMBER: US/09/782,816A  
 ; CURRENT FILING DATE: 2001-02-14  
 ; NUMBER OF SEQ ID NOS: 55  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 54  
 ; LENGTH: 183  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; US-09-782-816A-54

Query Match 97.8%; Score 135; DB 10; Length 183;  
 Best Local Similarity 96.7%; Pred. No. 8.7e-11;  
 Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEKIKTTVKESEATEEKLTIVPLAKOAL 30  
 Db 116 EVEKIKTTVKESEATEEKLTIVPLAKOAL 145

RESULT 7  
 US-10-425-115-3-15831  
 ; Sequence 315831, Application US/10425115  
 ; Publication No. US20040214272A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovacic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Current Application Number: US/10/425,115  
 ; FILE REFERENCE: 38-21(5322)B  
 ; TITLE OF INVENTION: Plants  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 369326  
 ; SEQ ID NO: 315831  
 ; LENGTH: 224  
 ; TYPE: PRT  
 ; ORGANISM: Zea mays  
 ; OTHER INFORMATION: Clone ID: MRT4577\_51109C.1.pep  
 ; US-10-425-115-3-15831

Query Match 97.8%; Score 135; DB 16; Length 224;  
 Best Local Similarity 96.7%; Pred. No. 1.1e-10;  
 Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEKIKTTVKESEATEEKLTIVPLAKOAL 30  
 Db 69 EVEKIKTTVKESEATEEKLTIVPLAKOAL 98

RESULT 8  
 US-09-782-816A-51  
 ; Sequence 51, Application US/09782816A  
 ; Publication No. US20030032771A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sharp, David J.

RESULT 9  
 US-09-782-816A-1  
 ; Sequence 1, Application US/09782816A  
 ; Publication No. US20030032771A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sharp, David J.  
 ; APPLICANT: Rogers, Gregory C.  
 ; APPLICANT: Scholey, Jonathon M.  
 ; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR PROLIFERATION  
 ; TITLE OF INVENTION: PROLIFERATION  
 ; CURRENT APPLICATION NUMBER: US/09/782,816A  
 ; CURRENT FILING DATE: 2001-02-14  
 ; NUMBER OF SEQ ID NOS: 55  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 1  
 ; LENGTH: 23  
 ; TYPE: PRT  
 ; ORGANISM: Unknown  
 ; FEATURE:  
 ; NAME/KEY: UNSURE  
 ; LOCATION: 22  
 ; OTHER INFORMATION: Xaa = Val or Ieu  
 ; OTHER INFORMATION: The sequence is a Homo sapiens sequence when Xaa  
 ; OTHER INFORMATION: represents Leu and a Mus musculus sequence when  
 ; OTHER INFORMATION: Xaa represents Val.  
 ; US-09-782-816A-1

Query Match 74.6%; Score 103; DB 10; Length 23;  
 Best Local Similarity 95.7%; Pred. No. 2.3e-07;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVEKIKTTVKESEATEEKLTIVPL 23  
 Db 1 EVEKIKTTVKESEATEEKLTIVPL 23

RESULT 10  
 US-10-501-282-4734  
 ; Sequence 4734, Application US/10501282  
 ; Publication No. US20050203280A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McMichael, John Calhoun

**APPLICANT:** ZAGURSKY, ROBERT JOHN  
**APPLICANT:** RUSSELL, DAVID PARRISH  
**APPLICANT:** FLETCHER, LEAH DIANE  
**TITLE OF INVENTION:** ALLOIACCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING  
**TITLE OF INVENTION:** POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF  
**FILE NUMBER:** PCT/US02/36123  
**CURRENT APPLICATION NUMBER:** US/10/501,282  
**CURRENT FILING DATE:** 2004-07-09  
**PRIOR APPLICATION NUMBER:** 60/333,777  
**PRIOR FILING DATE:** 2001-11-29  
**PRIOR APPLICATION NUMBER:** 60/426,742  
**PRIOR FILING DATE:** 2002-11-18  
**PRIOR APPLICATION NUMBER:** PCT/US02/36123  
**PRIOR FILING DATE:** 2002-11-25  
**NUMBER OF SEQ ID NOS:** 6653  
**SOFTWARE:** PatentIn version 3.2  
**SEQ ID NO:** 4734  
**LENGTH:** 334  
**TYPE:** PRT  
**ORGANISM:** Alloioaccus otitidis  
**RESULT** 11  
**S-10-501-282-4734**  
**Query Match** 40.6%; **Score** 56; **DB** 18; **Length** 334;  
**Best Local Similarity** 34.5%; **Pred.** No. 21; **Matches** 10; **Matches** 10; **Conservative** 11; **Mismatches** 8; **Indels** 0; **Gaps** 0;  
**GENERAL INFORMATION:**  
**APPLICANT:** DOUGLAS SMITH et al  
**TITLE OF INVENTION:** NUCLEIC ACID AND AMINO ACID SEQUENCES  
**RELATING TO HELICOBACTER PYLORI FOR**  
**DIAGNOSTICS AND THERAPEUTICS**  
**NUMBER OF SEQUENCES:** 10031  
**CORRESPONDENCE ADDRESS:**  
**ADDRESSEE:** LAHIVE & COCKFIELD  
**STREET:** 28 State Street  
**CITY:** Boston  
**STATE:** Massachusetts  
**COUNTRY:** USA  
**ZIP:** 02109-1875  
**COMPUTER READABLE FORM:**  
**MEDIUM TYPE:** CD-ROM ISO9660  
**COMPUTER:** IBM PC Compatible  
**OPERATING SYSTEM:** Windows NT 4.0  
**CURRENT APPLICATION DATA:**  
**APPLICATION NUMBER:** US/10/335,977  
**FILING DATE:** 30-Dec-2002  
**PRIOR APPLICATION DATA:**  
**APPLICATION NUMBER:** 08/993,002  
**ATTORNEY/AGENT INFORMATION:**  
**NAME:** Mandragoras, Amy E.  
**REGISTRATION NUMBER:** 36,207  
**REFERENCE/DOCKET NUMBER:** GTN-018  
**TELECOMMUNICATION INFORMATION:**  
**TELEPHONE:** (617) 227-7400  
**TELEFAX:** (617) 442-4214  
**INFORMATION FOR SEQ ID NO:** 7239  
**SEQUENCE CHARACTERISTICS:**  
**LENGTH:** 447 amino acids  
**TYPE:** amino acid  
**TOPOLOGY:** linear  
**MOLECULE TYPE:** protein  
**HYPOTHETICAL:** YES

Db 222 LKQFVRSACKELLTPPIAFKSM 244 ; PRIOR FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO: 20606  
; LENGTH: 10917  
; TYPE: PRT  
; ORGANISM: Streptomyces nodosus  
; US-10-732-923-20606  
; Query Match 37.0%; Score 51; DB 17; Length 10917;  
; Best Local Similarity 46.2%; Pred. No. 6.4e+03;  
; Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haelebeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Travick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forayth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.03A  
; CURRENT APPLICATION NUMBER: US11/0/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 6/0191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 6/0207,727  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 6/0206,848  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 6/0242,578  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 6/0230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 6/0230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 6/0267,636  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 6/0253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 6/0257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 6/0267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 6/0269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78514  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 47253  
; LENGTH: 932  
; TYPE: PRT  
; ORGANISM: Borrelia burgdorferi  
; US-10-282-122A-47253  
; RESULT 14  
; Query Match 37.0%; Score 51; DB 15; Length 932;  
; Best Local Similarity 37.9%; Pred. No. 3.e+02;  
; Matches 11; Conservative 6; Mismatches 12; Indels 0; Gaps 0;  
; QY 2 VEKIKTTVKESETBEKULTPVLLAKQAL 30  
; DB 397 IVDKDIDATEKYYIINKLTPFLAQPEGM 425  
; Search completed: November 3, 2005, 22:11:39  
; Job time : 56.0642 secB  
; US-10-732-923-20606  
; Sequence 20606, Application US/10732923  
; Publication No. US20050108791A1  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52/96)C  
; CURRENT APPLICATION NUMBER: US/10/732,923  
; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154

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GenCore version 5.1.6  
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## OM protein - protein search, using BW model

Run on: November 3, 2005, 21:32:33 ; Search time 71.1872 Seconds  
 (Without alignments)

282.516 Million cell updates/sec

Title: 09782816-3-1-22

Perfect score: 251

Sequence: 1. GVKEIPQKTYQLRLHEWQEL.....ESATEEKLTIVLAKOLAAL 52

Scoring table: BLOSUM62

Gappen 10.0 , Gapext: 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_16Dec04; \*  
 1: geneseq1980s; \*  
 2: geneseq1990s; \*  
 3: geneseq2000s; \*  
 4: geneseq2001s; \*  
 5: geneseq2002s; \*  
 6: geneseq2003aa; \*  
 7: geneseq2003bg; \*  
 8: geneseq2004s; \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

## ALIGNMENTS

26	67	26.7	1448	6 ADA89551	Ada89551 Staphyloc
27	67	26.7	2478	4 AAU37374	Aau37374 Staphyloc
28	67	26.7	2478	4 AAU34220	Aau34220 Staphyloc
29	67	26.7	2478	6 ABJ19002	Abj19002 Pathogen
30	67	26.7	2478	6 ABM71899	Abm71899 Staphyloc
31	67	26.7	2481	6 ABU15838	Abu15838 Protein e
32	67	26.7	2481	7 ABR62804	ABR62804 Methicillin
33	65	26.3	13 5 ABP5977	Abp5977 Cellular	
34	66	26.3	386	6 ABU44043	Abu44043 Protein e
35	66	26.3	868	2 AAY37731	Aay37731 Protein e
36	65	25.3	1020	4 AAM79875	Aam79875 Human pro
37	65.5	26.1	207	4 AAB29754	Ab29754 Rice PNI-
38	65.5	26.1	1837	8 ADS43304	Ad843304 Bacterial
39	64	25.5	140	4 AAO12168	Aao1216 Human pol
40	64	25.5	151	3 ARW03725	Arw03725 Human sec
41	64	25.5	188	2 AAW6545	Aaw6545 Human sto
42	64	25.5	188	3 AAB10278	Abi10278 Human fet
43	64	25.5	188	4 AAU12172	Aau12172 Human PRO
44	64	25.5	188	6 ABO17616	Abol17616 Novel PRO
45	64	25.5	188	6 ABU80870	Abu80870 Human PRO

Maximum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04; \*

1: geneseq1980s; \*

2: geneseq1990s; \*

3: geneseq2000s; \*

4: geneseq2001s; \*

5: geneseq2002s; \*

6: geneseq2003aa; \*

7: geneseq2003bg; \*

8: geneseq2004s; \*

Result No.: Score Query Match Length DB ID Description

1 251 100.0 314 8 ABB81421 Abm01421 Tumour-as

2 251 100.0 378 6 ABP98851 Abp98851 Human str

3 251 100.0 401 7 ADJ65563 Adj65563 Human hea

4 251 100.0 406 5 ABP53018 Abp53018 Human p50

5 251 100.0 465 3 AAB59968 Abp8968 Breast an

6 248 98.8 183 5 ABP53019 Abp53019 Mouse p50

7 246 98.8 183 5 ABP50106 Abp50106 Cellular

8 231 92.0 134 4 AAG75956 Aag75956 Human col

9 113 45.0 22 5 ABP52968 Abp52968 Cellular

10 107 42.6 21 5 ABP52969 Abp52969 Cellular

11 103 41.0 20 5 ABP52970 Abp52970 Cellular

12 103 41.0 23 5 ABP52966 Abp52966 Cellular

13 98 39.0 19 5 ABP52971 Abp52971 Cellular

14 93 37.1 18 5 ABP52972 Abp52972 Cellular

15 88 35.1 17 4 ABP52973 Abp52973 Cellular

16 81 32.3 16 5 ABP52974 Abp52974 Cellular

17 76 30.3 15 5 ABP52975 Abp52975 Cellular

18 72.5 28.9 53 5 ABP52977 Abp52977 Cellular

19 72.5 28.9 380 4 ABP52988 Abp52988 Drosophi

20 72.5 28.9 380 5 ABP53020 Abp53020 Drosophi

21 71 28.3 14 5 ABP52976 Abp52976 Cellular

22 70 27.9 1087 4 ABP65359 Abp65359 Drosophi

23 70 27.9 1087 4 ABP65358 Abp65358 Drosophi

24 68 27.9 2368 4 AAU34139 Aau34139 Staphyloc

25 68 27.1 2368 4 AAU36796 Aau36796 Staphyloc

## RESULT 1

ABMB1421

ID ABMB1421 standard; protein; 314 AA.

XX

AC ABMB1421;

DT 18-NOV-2004 (first entry)

XX

DB Tumour-associated antigenic target (TAT) polypeptide PRO82191, SEQ:3675.

XX

DR

Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic.

XX

KW

PT  
XX  
PS  
XX  
SQ  
Claim 1; Page 298; 361pp; English.

This sequence represents a novel isolated human structural and cytoskeleton-associated protein (SCAP) polypeptide. The polypeptides and poly nucleotides encoding them are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or over expression of SCAP, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's disease, stroke), heart (e.g. hypertension, heart failure, angina) and skeletal muscle disorders (e.g. osteoporosis, osteoarthritis) or viral infections. These are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of SCAP. The SCAP or its fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. The microarray is useful in monitoring or measuring protein-protein interactions, drug-target interactions, and gene expression profiles

Sequence 378 AA;

PT with the disease.

XX  
PS Claim 1; SEQ ID NO 1369; 180pp; English.

CC This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are present for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy and ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.

CC mitochondrial protein of the invention.  
CC cytoskeletal activities. This polypeptide sequence is a human heart  
CC mitochondrial protein of the invention.  
CC mitochondrial protein of the invention.

SQ Sequence 401 AA;

Query Match 100.0%; Score 251; DB 7; Length 401;  
Best Local Similarity 100.0%; Pred. No. 7.9e-21; Mismatches 52;  
Matches 52; Conservative 0; Indels 0; Gaps 0;

QY 1 GVKEPQQKQYQRLIHEVQELTEVEKIKITVKESATEKUTPVILAKQLAL 52  
Db 94 GVKEPQQKQYQRLIHEVQELTEVEKIKITVKESATEKUTPVILAKQLAL 145

RESULT 4

ABB53018 ABP53018 standard; protein; 406 AA.

XX AC ABB53018;

XX DT 05-NOV-2002 (first entry)

DE Human p50 amino acid sequence SEQ ID NO:53.

XX

XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; KW p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; KW sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder; KW glial disorder; astrocytial disorder; hypothalamic disorder; inflammatory; KW stromal disorder; macrophagal disorder; epithelial disorder; KW immunologic disorder; blastocoelic disorder; angiogenic disorder; KW OS Homo sapiens.

XX OS Homo sapiens.

XX

PN WO200264779-A2.

XX PD 22-AUG-2002.

XX PP 21-JAN-2002; 2002WO-US001708.

XX PR 14-FEB-2001; 2001US-00782816.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Sharp DJ, Rogers GC, Scholey JM;

XX DR WPI; 2002-657599/0.

XX PT New peptide inhibitors of p50/dynamitin useful for treating cancer by PT inhibiting cellular proliferation, e.g. benign or malignant tumors, PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and PT immunologic disorders.

XX PS Disclosure; Fig 1; 55pp; English.

CC The present invention describes an isolated peptide (I) comprising or

CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the CC sequences given in ABB296 and ABP5267 and can have C-terminal and N-terminal extensions. (1) have cytosstatic and antiinflammatory activities CC and can be used as p50/dynamitin inhibitors and methods from the present invention CC peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such CC as benign or malignant tumours (renal, liver, kidney, bladder, breast, CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such CC as neuronal, glial, astrocytal, hypothalamic and other glandular, CC macrophagal, epithelial, stromal and blastocoelic disorders; and CC inflammatory, angiogenic and immunologic disorders. The present sequence CC represents human p50 which is given in the exemplification of the present invention

SQ Sequence 406 AA;

Query Match 100.0%; Score 251; DB 5; Length 406;  
Best Local Similarity 100.0%; Pred. No. 8.1e-21; Mismatches 52;  
Matches 52; Conservative 0; Indels 0; Gaps 0;

QY 1 GVKEPQQKQYQRLIHEVQELTEVEKIKITVKESATEKUTPVILAKQLAL 52  
Db 99 GVKEPQQKQYQRLIHEVQELTEVEKIKITVKESATEKUTPVILAKQLAL 150

RESULT 5

ABB5968 ABB5968 standard; protein; 465 AA.

XX AC ABB5968;

XX DT 27-MAR-2001 (first entry)

XX DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 676.

XX Human; breast cancer; ovarian cancer; cytostatic; immuno suppressive; KW nootropic; neuroprotective; antiviral; antiallergic; hepatotrophic; KW antibacterial; antiinflammatory; antiulcer; vasoconstrictor; KW antidiabetic; antifungal; antiparasitic; cardiant; immune disorder; KW autoimmune disease; allergy; autoimmune haemolytic anaemia; KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis; KW cardiovascular disorder; wound healing; neurological disease.

XX OS Homo sapiens.

XX PN WO200055173-A1.

XX PD 21-SEP-2000.

XX PP 08-MAR-2000; 2000WO-US00581.

XX PR 12-MAR-1999; 99US-0124270P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;

XX WPI; 2000-611515/58.

XX DR N-PSDB; AAF21871.

XX PT New human breast and ovarian cancer associated gene sequences and the

PT polyptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and

PT neurological diseases.

XX Claim 11; Page 1126-1128; 1299pp; English.

XX PS Sequences AAF21614 - AAF22031 represent DNA sequences encoding human

CC proteins AAB871 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are

CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the CC isolation and characterisation of the DNA and protein sequences of the CC invention. The breast and ovarian cancer associated DNA, protein, agonist CC or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; CC neuroprotective; antiviral; antiallergic; hepatoprotective; antidiabetic; CC antiinflammatory; antidiabetic; and cardiotonic activity. The polynucleotide and CC protein sequences are used in the diagnosis of cancer, particularly CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists CC and antagonists may also be used in the diagnosis, prevention and treatment CC of immune disorders e.g. Addison's disease, allergies, autoimmune CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; CC cardiovascular disorders such as myocardial ischaemias; wound healing; CC neurological diseases such as cerebral anoxia and epilepsy; and CC infectious diseases

XX SQ Sequence 465 AA;

Query Match 100.0%; Score 251; DB 3; Length 465; Best Local Similarity 100.0%; Pred. No. 9.4e-21; Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKE~~TPOQKYQRLHLHEVQE~~LTTVEKIKTVKESATEEKLT~~PV~~LAKQLAAL 52  
Db 158 GVKE~~TPOQKYQRLHLHEVQE~~LTTVEKIKTVKESATEEKLT~~PV~~LAKQLAAL 209

RESULT 6

ID ABP53019  
ID ABP53019 standard; protein; 183 AA.

AC XX ABP53019;  
XX

DT 05-NOV-2002 (first entry)

DB Mouse p50 amino acid sequence SEQ ID NO:54.

XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder; KW glial disorder; astrocytolar disorder; hypothalamic disorder; inflammatory; KW glandular disorder; macrophagal disorder; epithelial disorder; KW stromal disorder; blastocoelic disorder; angiogenic disorder; KW immunologic disorder.

OS Homo sapiens.

OS Mus musculus.

OS Synthetic.

OS Mus musculus.

PN WO200264779-A2.

PD 22-AUG-2002.

PP 21-JAN-2002; 2002WO-US001708.

PR 14-FEB-2001; 2001US-00782816.

XX PA (REGC ) UNIV CALIFORNIA.

PT Sharp DJ, Rogers GC, Scholey JM;

XX DR WPI; 2002-657599/70.

PT New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.

XX Disclosure; Fig 2; 55pp; English.

CC The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities

CC and can be used as p50/dynamitin inhibitors and in gene therapy. The CC peptides, nucleic acid molecules and methods from the present invention CC are useful for treating cancer by inhibiting cellular proliferation, such CC as benign or malignant tumours (renal, liver, kidney, bladder, breast, CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, head and CC neck tumours); leukaemias and lymphoid malignancies, other disorders such CC as neuronal, glial, astrocytal, hypothalamic and other glandular, CC macrophagal, epithelial, stromal and blastocoelic disorders; and CC inflammatory, angiogenic and immunologic disorders. The present sequence CC represents mouse p50 which is given in the exemplification of the present invention.

XX SQ Sequence 183 AA;

Query Match 98.8%; Score 249; DB 5; Length 183; Best Local Similarity 98.1%; Pred. No. 7.1e-21; Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKE~~TPOQKYQRLHLHEVQE~~LTTVEKIKTVKESATEEKLT~~PV~~LAKQLAAL 52  
Db 94 GVKE~~TPOQKYQRLHLHEVQE~~LTTVEKIKTVKESATEEKLT~~PV~~LAKQLAAL 145

RESULT 7

ID ABP53016

ID ABP53016 standard; peptide; 52 AA.

AC XX ABP53016;

DT 05-NOV-2002 (first entry)

DE Cellular proliferation peptide inhibitor SEQ ID NO:51.

XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;

KW p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma;

KW sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;

KW glial disorder; astrocytolar disorder; hypothalamic disorder; inflammatory;

KW stromal disorder; blastocoelic disorder; epithelial disorder;

KW immunologic disorder.

OS Homo sapiens.

OS Mus musculus.

OS Synthetic.

XX FH Key

FT Misc-difference 44

FT /label= Leu, Val

FT /note= "Leu in humans and Val in Mus musculus"

PN WO200264779-A2.

PD 22-AUG-2002.

XX PR 21-JAN-2002; 2002WO-US001708.

XX PR 14-FEB-2001; 2001US-00782816.

XX PA (REGC ) UNIV CALIFORNIA.

PT Sharp DJ, Rogers GC, Scholey JM;

XX DR WPI; 2002-657599/70.

PT New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.

PS Claim 2; Page 31; 55pp; English.

XX The present invention describes an isolated peptide (I) comprising or

CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP2966 and ABP52967 and can have C-terminal and N-terminal extensions. (1) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours); leukaemias and lymphoid malignancies; other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders; and inflammatory, angiogenic and immunologic disorders. The present sequence represents a specifically claimed peptide inhibitor of cellular proliferation from the present invention

XX Sequence 52 AA;

Query Match 98.0%; Score 246; DB 5; Length 52;  
Best Local Similarity 98.1%; Pred. No. 2.8e-21; Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVKETPQQKYQRLLHVEQLTTEVERKIKTVKESATEEKLTVPVLAQKAL 52  
Db 1 GVKETPQQKYQRLLHVEQLTTEVERKIKTVKESATEEKLTVPVLAQKAL 52

RESULT 8  
ID AAG75956 standard; protein; 134 AA.

XX AAG75956;  
AC DT 03-SEP-2001 (first entry)

XX Human colon cancer antigen protein SEQ ID NO:6720.  
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;  
KW colorectal carcinoma; chromosome 12.  
OS Homo sapiens.  
XX WO200122920-A2.  
XX PD 05-APR-2001.  
XX PP 28-SEP-2000; 2000WO-US026524.  
XX PR 29-SEP-1999; 99US-0157137P.  
XX PR 03-NOV-1999; 99US-0163280P.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PI Ruben SM, Barash SC, Birse CE, Rosen CA;  
XX DR WPI; 2001-235357/24.  
XX DR N-PSDB; AH35361.

PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.  
XX PS Claim 11; Page 8181; 9803PP; English.

XX CC AAH2943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytosstatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P, by expressing inactive proteins or to supplement the patient's own production of P. Additionally, N may be used

CC to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins N and P and can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N-B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922  
XX Sequence 134 AA;

Query Match 92.0%; Score 231; DB 4; Length 134;  
Best Local Similarity 100.0%; Pred. No. 4.8e-19; Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TPOQKYQRLLHVEQLTTEVERKIKTVKESATEEKLTVPVLAQKAL 48  
Db 1 TPOQKYQRLLHVEQLTTEVERKIKTVKESATEEKLTVPVLAQKAL 48

RESULT 9  
ID ABP52968 standard; peptide; 22 AA.

XX ABP52968;  
AC DT 05-NOV-2002 (first entry)

XX DE Cellular proliferation inhibitor related peptide SEQ ID NO:3.  
XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; hypotalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder; immunologic disorder.  
OS Homo sapiens.  
OS Mus musculus.  
OS Synthetic.  
XX PN WO200264779-A2.  
XX PD 22-AUG-2002.  
XX PP 21-JAN-2002; 2002WO-US001708.  
XX PR 14-FEB-2001; 2001US-00782816.  
XX PA (REGC ) UNIV CALIFORNIA.  
XX PI Sharp DJ, Rogers GC, Scholey JM;  
XX DR WPI; 2002-657599/70.  
XX PT New Peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukaemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.  
XX PS Claim 1; Page 29; 55pp; English.

XX CC The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP2965 and ABP52967 and can have C-terminal and N-terminal extensions. (1) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and

CC neck tumours); leukaemias and lymphoid malignancies, other disorders such  
 CC as neuronal, glial, astrocytal, hypothalamic and other glandular,  
 CC macrophagal, epithelial, stromal and blastocoelic disorders; and,  
 CC inflammatory, angiogenic and immunologic disorders. The present sequence  
 CC represents a peptide that can be N-terminally added to (P1)

SQ Sequence 22 AA;

Query Match 45.0%; Score 113; DB 5; Length 22;

Best Local Similarity 100.0%; Pred. No. 3.4e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVKETPQQKYORLHLHEVQLTT 22

Db 1 VKEPTPQQKYORLHLHEVQLTT 22

RESULT 10

ABP52969 ID ABP52969 standard; Peptide; 21 AA.

XX AC

XX DT

05-NOV-2002 (first entry)

DB Cellular proliferation inhibitor related peptide SEQ ID NO:4.

XX DE

XX KW

XX OS

OS Mus musculus.

OS Synthetic.

XX PN

PN WO200264779-A2.

XX PD

PD 22-AUG-2002.

XX PR

PR 21-JAN-2002; 2002WO-US001708.

XX PR

PR 14-FEB-2001; 2001US-00782816.

XX PA

(REGC ) UNIV CALIFORNIA.

XX PI

PI Sharp DJ, Rogers GC, Scholey JM;

XX PT

PT Sharp DJ, Rogers GC, Scholey JM;

CC inflammatory, angiogenic and immunologic disorders. The present sequence  
 CC represents a peptide that can be N-terminally added to (P1)  
 SQ Sequence 21 AA;

Query Match 42.6%; Score 107; DB 5; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.6e-05; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKEPTPQQKYORLHLHEVQLTT 22

Db 1 VKEPTPQQKYORLHLHEVQLTT 21

RESULT 11

ABP52970 ID ABP52970 standard; peptide; 20 AA.

XX AC

XX DT

05-NOV-2002 (first entry)

DB Cellular proliferation inhibitor related peptide SEQ ID NO:5.

XX DE

XX KW

OS Homo sapiens.

OS Mus musculus.

OS Synthetic.

XX PN

PN WO200264779-A2.

XX PD

PD 22-AUG-2002.

XX PR

PR 21-JAN-2002; 2002WO-US001708.

XX PR

PR 14-FEB-2001; 2001US-00782816.

XX PA

(REGC ) UNIV CALIFORNIA.

XX PI

PI Sharp DJ, Rogers GC, Scholey JM;

XX PT

PT Sharp DJ, Rogers GC, Scholey JM;

XX PT

PT WPI; 2002-657599/70.

XX PT

PT New peptide inhibitors of p50/dynamitin useful for treating cancer by  
 PT inhibiting cellular proliferation, e.g. benign or malignant tumors,  
 PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and  
 PT immunologic disorders.

XX PS

PS Claim 1; Page 29; 55pp; English.

XX CC

CC The present invention describes an isolated peptide (I) comprising or  
 CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the  
 CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-  
 CC terminal extensions. (I) have cytostatic and antiinflammatory activities  
 CC and can be used as p50/dynamitin inhibitors and in gene therapy. The  
 CC peptides, nucleic acid molecules and methods from the present invention  
 CC are useful for treating cancer by inhibiting cellular proliferation, such  
 CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,  
 CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, bladder, breast,  
 CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and  
 CC neck tumours); leukaemias and lymphoid malignancies, other disorders such  
 CC as neuronal, glial, astrocytal, hypothalamic and other glandular,  
 CC macrophagal, epithelial, stromal and blastocoelic disorders; and  
 CC inflammatory, angiogenic and immunologic disorders. The present sequence  
 CC represents a peptide that can be N-terminally added to (P1)

XX CC

CC represents a peptide that can be N-terminally added to (P1)

SQ	Sequence 20 AA;
Query Match	41.0%; Score 103; DB 5; Length 20;
Best Local Similarity	100.0%; Pred. No. 4.5e-05;
Matches	20; Conservative 0; Mismatches 0;
OY	3. KEPPOQKYQRLHEVQLTT 22
DB	1 KEPPOQKYQRLHEVQLTT 20
RESULT 12	
ID	ABP52966
ID	ABP52966 standard; peptide; 23 AA.
AC	ABP52966;
XX	
DT	05-NOV-2002 (first entry)
XX	
DB	Cellular proliferation inhibitor related peptide SEQ ID NO:1.
XX	
CC	Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KW	p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma;
KW	sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;
KW	glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KW	glandular disorder; macrophagal disorder; epithelial disorder; inflammatory;
KW	stromal disorder; blastocoelic disorder; angiogenic disorder;
KW	immunologic disorder.
XX	
OS	Homo sapiens.
OS	Mus musculus.
OS	Synthetic.
XX	
FH	
FT	Location/Qualifiers
FT	Misc-difference 22
FT	/label= "Leu, Val
FT	/notes= "Leu in humans and Val in Mus musculus"
PN	WO200264779-A2.
XX	
PD	22-AUG-2002.
XX	
PR	21-JAN-2002; 2002WO-US001708.
XX	
PR	14-FEB-2001; 2001US-00782816.
XX	
PA	(REGC ) UNIV CALIFORNIA.
XX	
PT	Sharp DJ, Rogers GC, Scholey JM;
XX	
PT	WPI; 2002-657599/70.
XX	
PT	New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.
XX	
PT	New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.
XX	
PS	Claim 1; Page 29, 55pp; English.
PS	The present invention describes an isolated peptide (1) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (1) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders; and inflammatory, angiogenic and immunologic disorders.
CC	The present sequence represents a peptide that can be N-terminally added to (P1).
CC	Sequence 19 AA;
RESULT 13	
ID	ABP52971
ID	ABP52971 standard; peptide; 19 AA.
XX	
AC	ABP52971;
XX	
DT	05-NOV-2002 (first entry)
XX	
DB	Cellular proliferation inhibitor related peptide SEQ ID NO:6.
XX	
CC	Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KW	p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma;
KW	sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;
KW	glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KW	glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder;
KW	immunologic disorder.
XX	
OS	Homo sapiens.
OS	Mus musculus.
OS	Synthetic.
XX	
DN	WO200264779-A2.
XX	
PD	22-AUG-2002.
XX	
PP	21-JAN-2002; 2002WO-US001708.
XX	
PR	14-FEB-2001; 2001US-00782816.
XX	
PA	(REGC ) UNIV CALIFORNIA.
XX	
PT	Sharp DJ, Rogers GC, Scholey JM;
XX	
DR	WPI; 2002-657599/70.
XX	
PT	New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.
XX	
PS	Claim 1; Page 29, 55pp; English.
PS	The present invention describes an isolated peptide (1) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (1) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders; and inflammatory, angiogenic and immunologic disorders.
CC	The present sequence represents a peptide that can be N-terminally added to (P1).
CC	Sequence 19 AA;

Query Match 39.0%; Score 98; DB 5; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 0.00016; Mismatches 0; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TPQQKYQRULHEVQELTT 22  
 Db 1 TPQQKYQRULHEVQELTT 19

RESULT 14  
 ABP52972  
 ID ABP52972 standard; peptide; 18 AA.  
 AC ABP52972;  
 XX DT 05-NOV-2002 (first entry)

XX Cellular proliferation inhibitor related peptide SEQ ID NO:7.

DB XX Cellular proliferation inhibitor related peptide SEQ ID NO:8.

XX Cellular proliferation inhibitor related peptide SEQ ID NO:9.

XX Cellular proliferation inhibitor; cytostatic; antiinflammatory; cancer; sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory; stromal disorder; blastocoelic disorder; epithelial disorder; immunologic disorder.

XX KW Homo sapiens.

XX OS Mus musculus.

OS Synthetic.

XX PN WO200264779-A2.

XX PD 22-AUG-2002.

XX PR 21-JAN-2002; 2002WO-US001708.

XX PR 14-FEB-2001; 2001US-00782816.

XX PA (REGC ) UNIV CALIFORNIA.

XX PT Sharp DJ, Rogers GC, Scholey JM; DR

XX PR WPI; 2002-657599/70.

PT New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.

PT New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.

PT New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.

PS XX Claim 1; Page 29; 55pp; English.

CC CC The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumors (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders; and inflammatory, angiogenic and immunologic disorders. The present sequence represents a peptide that can be N-terminally added to (P1).

SQ XX Sequence 18 AA;

Query Match 37.1%; Score 93; DB 5; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 0.00058; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 39.0%; Score 98; DB 5; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 0.00016; Mismatches 0; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 5 TPQQKYQRULHEVQELTT 22  
 Best Local Similarity 100.0%; Pred. No. 0.0021; Mismatches 0; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 35.1%; Score 88; DB 5; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.0021; Mismatches 0; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Mon Nov 7 09:42:36 2005

Db 1 PQQKYQRLLHEVQELTT 17

Search completed: November 3, 2005, 21:57:29  
Job time : 73.1872 secs

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Om protein - protein search, using sw model

Run on: November 3, 2005, 21:43:09 ; Search time 18.9091 Seconds  
 (without alignments)  
 264.596 Million cell updates/sec

Title: Perfect score: 251  
 Sequence: 1 GVKETPQQKQRQLHVEQEL.....ESATEEKLTPVLLAKQAL 52  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9616763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match Length	DB ID	Description	
1	69.5	27.7	804	T32864	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
2	68	27.1	1742	T4951	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
3	67.5	26.9	1325	S16129	Caenorhabditis elegans
4	67	26.7	1287	T22235	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
5	67	26.7	2481	D90011	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
6	66	26.3	393	T04957	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
7	66	26.3	866	C71309	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
8	65.5	26.1	1837	T41023	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
9	64	25.5	210	E84499	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
10	63.5	25.3	163	S69518	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
11	63.5	25.3	374	D70391	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
12	63	25.1	281	F75216	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
13	63	25	314	F90577	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
14	62.5	24.9	1281	JC3368	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
15	62	24.7	296	T32222	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
16	62	24.7	2469	H3612	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
17	61	24.3	442	C95070	sensor histidine kinase
18	61	24.3	442	A97938	histidine kinase
19	60.5	24.1	819	AC2029	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
20	60.5	24.1	1214	JC2069	zinc-finger protein
21	60	23.9	523	S05920	glucose transport
22	60	23.9	695	H72243	translation elongation factor
23	59.5	23.7	279	D71453	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
24	59.5	23.7	665	S62328	kinesin-like DNA binding protein
25	59	11.2	112	G72445	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
26	59	23.5	239	D84004	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
27	59	23.5	550	G85336	hypothetical protein ZK484.4 - <i>Caenorhabditis elegans</i>
28	59	611	2	E90543	glucose inhibited protein ZK484.4 - <i>Caenorhabditis elegans</i>
29	59	23.5	782	A34219	D-protein - fr

RESULT 2

T4951  
 kinase-like protein Kif21a related protein [imported] - *Neurospora crassa*  
 N;Alternative names: protein Bl4D6\_30  
 C;Species: *Neurospora crassa*  
 C;Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
 C;Accession: T4951  
 R;Schulte, U.; Aign, V.; Hohisel, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura, A.;Reference number: Z25022  
 A;Accession: T49451  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residue: 1-1742 <SCH>  
 A;Cross-references: UNIPROT:Q8X0C5; EMBL:ATJ356173; GSPDB:GN00116; NCSP:B14B6\_30  
 A;Experimental source: BAC clone Bl4D6; strain OR74A  
 C;Genetics:

A;Gene: NCSP:BL14D6.30  
A;Map position: 6  
A;Introns: 58/1; 166/1; 267/3; 1543/3  
Query Match 27.1%; Score 68; DB 2; Length 1742;  
Matches 15; Conservative 8; Mismatches 18; Indels 0; Gaps 0;  
Oy 7 QOKYORLHEVOELTTEVEKIKTVKESATEEKLTPLVLLAK 47  
Db 950 EBKHOETLDMWEELEKIAKQALSVESSISRTSTPVIRK 990

**RESULT 3**

S16129 dynein-associated protein, 150K, cytosolic - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S16129  
R;Holzbaur, E.I.F.; Hammarback, J.A.; Paschal, B.M.; Kravit, N.G.; Pfister, K.K.; Vallee  
Nature 351, 579-583, 1991.  
A;Title: Homology of a 150K cytoplasmic dynein-associated polypeptide with the Drosophil  
A;Reference number: S16129; MUID:91260877; PMID:1828535  
A;Accession: S16129  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1325 <KRV>  
A;Cross-references: UNIPROT:P28023

Query Match 26.9%; Score 67.5; DB 2; Length 1325;  
Best Local Similarity 34.7%; Pred. No. 56;  
Matches 17; Conservative 11; Mismatches 20; Indels 1; Gaps 1;  
Oy 1 VKETPQQKQYORLHEVOELTTEVEKIKTVKESATEEKLTPLVLLAK 49  
Db 314 GAESIQQEVALKERVDLTTIDBLIKEEKGSDGAASSYQI-KQL 361

**RESULT 4**

T22235 hypothetical protein R45G2.3 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Accession: T22235  
R;Lindsay, S.  
submitted to the EMBL Data Library, March 1997  
A;Reference number: Z19535  
A;Accession: T22235  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1287 <WIL>  
A;Cross-references: UNIPROT:O62245; EMBL:Z93382; PIDN:CAB07612.1; GSPDB:GN00021; CESP:F4  
A;Experimental source: clone R45G2  
C;Genetics:

A;Gene: CESP:45G2.3  
A;Map position: 3  
A;Introns: 59/2; 117/3; 153/3; 180/2; 233/2; 341/3; 393/1; 424/2; 551/3; 664/3; 734/3; 8

Query Match 26.7%; Score 67; DB 2; Length 1287;  
Best Local Similarity 31.6%; Pred. No. 61; Mismatches 18; Conservative 11; Indels 10; Gaps 2;  
Matches 18; Conservative 11; Mismatches 18; Indels 10; Gaps 2;

Oy 4 ETPOQKQYORLHEVOELTTEVEKIKTVKESATEEKLTPLVLLAK 50  
Db 1122 EPPPEKKQKULLEVDDDFSERFQEKVNTKESVAEKKVENSNEELKPPPIRKAVS 1178

**RESULT 5**

D90011 FmtB protein [imported] - *Staphylococcus aureus* (strain N315)  
C;Species: *Staphylococcus aureus*  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C;Accession: D90011

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi  
ma, A.; Mizutani-Ul, Y.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I  
C.; Shiba, T.; Hattori, M.; Ogawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001.  
A;Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.  
A;Accession: D90011  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-2481 <KUR>  
A;Cross-references: UNIPROT:Q99066; GB:BA000018; PIDN:BAB43253.1; GSPDB:Gi  
A;Experimental source: strain N315  
C;Genetics:  
A;Gene: fmbB(mrp)

Query Match 26.7%; Score 67; DB 2; Length 2481;  
Best Local Similarity 35.1%; Pred. No. 1.2e+02; Mismatches 15; Indels 0; Gaps 0;  
Matches 13; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

Oy 2 VKETPQQKQYORLHEVOELTTEVEKIKTVKESATEEKLTPLVLLAK 38  
Db 1609 IEQPNNASQEINDAQEVDTELNQAKINVDQSSTNE 1645

**RESULT 6**

T04957 hypothetical protein F7J7.200 - *Arabidopsis thaliana*  
C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C;Accession: T04957  
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Badgerot, I.; Mewes, H.W.; Mayer, K.F.X.  
submitted to the Protein Sequence Database, July 1998  
A;Reference number: Z15391  
A;Accession: T04957  
A;Molecule type: DNA  
A;Residues: 1-393 <BEV>  
A;Cross-references: UNIPROT:O49667; EMBL:AL021960  
A;Experimental source: cultivar Columbia; BAC clone F7J7  
A;Genetics:  
A;Map position: 4  
A;Introns: 80/1; 217/3; 264/1; 291/3  
A;Note: F7J7.200

Query Match 26.3%; Score 66; DB 2; Length 393;  
Best Local Similarity 38.6%; Pred. No. 21; Mismatches 12; Indels 7; Gaps 8; Gaps 2;

Oy 3 KETPQQKQYORLHEVOELTTEVEKIKTVKESATEEKLTPLVLL 45  
Db 27 QESTQQTHQNLKYQ-----KWRSTLQDSDAELKLSPALV 63

**RESULT 7**

C71509 probable DNA polymerase I - *Chlamydia trachomatis* (serotype D, strain UW3/Cx)  
C;Species: *Chlamydia trachomatis*  
C;Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004  
C;Accession: C71509  
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,  
Science 282, 754-759, 1998.  
A;Title: Genome sequence of an obligate intracellular pathogen of humans: *Chlamydia traci*  
A;Reference number: A71570; MUID:9900809; PMID:9784136  
A;Accession: C71509  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-866 <ARN>  
A;Cross-references: UNIPROT:O84500; GB:AE001322; GB:AE001273; NID:93328916; PIDN: AAC6809  
A;Experimental source: serotype D, strain UW-3/Cx  
C;Genetics:  
A;Gene: polA  
C;Superfamily: DNA-directed DNA polymerase I  
Query Match 26.3%; Score 66; DB 2; Length 866;

Best Local Similarity 36.4%; Pred. No. 50; Matches 20; Conservative 10; Mismatches 21; Indels 4; Gaps 2; Score 24

RESULT 8

Unprobable nuclear pore complex-associated protein - fission yeast (Schizosaccharomyces pombe) [Species: Schizosaccharomyces pombe]; Accession: T41023

Query Match 25.5%; Score 64; DB 2; Length 210; Best Local Similarity 40.5%; Pred. No. 17; Matches 17; Conservative 9; Mismatches 14; Indels 2; Gaps 2; Status: preliminary; Molecule type: DNA; Residues: 1-1837 <MUR>

Cross-references: UNIPROT:074424; EMBL:AL0239860; PIDN:CRA19588.1; GSPDB:GN00068; SPDB:SPCC162.08C

Experimental source: strain 972h-; cosmid c162

Genetics: Map position: 3

Accession: T41023

Submitted to the EMBL Data Library, June 1998

Reference number: Z221965

Accession: T41023

Status: preliminary; translated from GB/EMBL/DDJB

Residues: 1-1837 <MUR>

Local Similarity 37.8%; Pred. No. 15; Mismatches 11; Indels 1; Gaps 1; Score 24

Best Local Similarity 37.8%; Pred. No. 15; Mismatches 11; Indels 1; Gaps 1; Score 24

Query Match 26.1%; Score 65.5; DB 2; Length 1837; Best Local Similarity 35.8%; Pred. No. 1.3e+02; Matches 19; Conservative 10; Mismatches 17; Indels 7; Gaps 2; Score 24

QY 7 PQKXORLHLHEVQLTTEVEKIK-TTVKESATEEKLTPVLAKQ 48

Db 662 QTSYQRSLRLEQTLNELESLKSISRNKEKKFEEAISILOEKSNIQQLQTSL 714

RESULT 9

hypothetical protein At2g1890 [imported] - Arabidopsis thaliana (mouse-ear cress)

Accession: E84499

Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 12-Jul-2004

Query Match 25.3%; Score 63.5; DB 2; Length 163; Best Local Similarity 37.8%; Pred. No. 15; Mismatches 11; Indels 1; Gaps 1; Score 24

QY 5 TPQQKXORLHLHEVQLTTEVEKIK-TTVKESATEEKLTPVLAKQ 48

Db 25 TPQKOFIKLMEFGELCSGVAKKNPDVKDSIGCFVVMVILAKQ 69

RESULT 10

hypothetical protein At2g1890 [imported] - Arabidopsis thaliana (mouse-ear cress)

Accession: E84499

Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 12-Jul-2004

Query Match 25.3%; Score 63.5; DB 2; Length 163; Best Local Similarity 37.8%; Pred. No. 15; Mismatches 11; Indels 1; Gaps 1; Score 24

QY 6 PQKXORLHLHEVQLTTEVEKIK-TTVKESATEEKLTPVLAKQ 51

Db 164 PRKRCPEEVDTNLKYLHENEYLEKSIQEINTTEKRAKGKI-ENARNEFKTEELKELSS 222

RESULT 11

hypothetical protein ag1060 - Aquifex aeolicus

Accession: D70391

Species: Aquifex aeolicus

Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004

Query Match 25.3%; Score 63.5; DB 2; Length 374; Best Local Similarity 31.1%; Pred. No. 36; DB 2; Length 374; Matches 19; Conservative 14; Mismatches 13; Indels 15; Gaps 3; Score 24

QY 6 PQKXORLHLHEVQLTTEVEKIK-TTVKESATEEKLTPVLAKQ 51

Db 52 L 52

Db 223 L 223

RESULT 12

hypothetical protein PAB2181 - Pyrococcus abyssi (strain Orsay)

Accession: F75216

Species: Pyrococcus abyssi

Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004

Query Match 25.5%; Score 64; DB 2; Length 210; Best Local Similarity 40.5%; Pred. No. 17; Matches 17; Conservative 9; Mismatches 14; Indels 2; Gaps 2; Status: preliminary; Molecule type: DNA; Residues: 1-210 <STO>

Cross-references: UNIPROT:Q9SIY3; GB:AB002093; NID:94557062; PIDN:AAD22501.1; GSPDB:GN00068

Genetics: Map position: 2

Superfamily: uncharacterized CTH domain protein

Accession: F75216

Submitted to the EMBL Data Library, July 1999

Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure

Reference number: A75001

Accession: F75216

Status: preliminary; Genoscope

Molecule type: DNA

Residues: 1-281 <KAM>

Cross-references: UNIPROT:Q9V217; GB:AJ248283; GB:AL096836; NID:95457433; PIDN:CAB4918

Experimental source: strain Orsay

Genetics: FAB2181

Result 169518

Hypothetical protein 12 - phage HPI

Species: phage HPI

Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

Accession: S69518

Query Match 25.1%; Score 63; DB 2; Length 281;

Best Local Similarity 36.6%; Pred. No. 30; Matches 15; Conservative 12; Mismatches 12; Indels 2; Gaps 2;

Qy 1 GVK-E-TPOQKVQLRHEVQSLTTEVKIKTVKSSATEEKL 40  
Db 119 GIKEVWVAREEYEKLUKEYEKUQEFEEVKARI-TAAELESI 158

RESULT 13

F90577 lipoprotein vaab [Imported] - Mycoplasma pulmonis (strain UAB CTIP) (fragment)

C;Species: Mycoplasma pulmonis

C;Accession: F90577 Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004

C;Accession: F90577 Reference number: A99512; MUID:21267165; PMID:11353084

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-296 <DAV>

A;Cross-references: UNIPROT:O17002; EMBL:AF022382; PIDN:AAB69938.1; GSPDB:GN00023; CESP:

A;Experimental source: strain Bristol N2; clone T23P12

C;Genetics: CESP;r23B12.7

A;Gene: CESP;T23B12.7

A;Map position: 5

A;Intron: 67/3

Query Match 25.1%; Score 63; DB 2; Length 314;

Best Local Similarity 29.8%; Pred. No. 34; Matches 14; Conservative 17; Mismatches 10; Indels 6; Gaps 2;

Qy 2 WKETPQQKYQRLHRLH---VQBLTEVEKIKTVKSSATEEKLTVL 44  
Db 246 ITEEQAKFKVVIQDARTKLUQDLITKLEKIKS--EKENIEKLDPII 290

RESULT 14

JC5368 dynactin 1 - mouse  
N;Alternate names: p150 Glued  
C;Species: Mus musculus (house mouse)  
C;Date: 28-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 09-Jul-2004

C;Accession: JC5368 Reference number: JC5368; MUID:97223454; PMID:9070275

R;Jang, W.; Weber, J.S.; Tokito, M.K.; Holzbaur, E.L.F.; Meisler, M.H.

Biochem. Biophys. Res. Commun. 231: 341-347, 1997

A;Title: Mouse p150Glued (dynactin 1) cDNA sequence and evaluation as a candidate for th

A;Accession: JC5368  
A;Gene: Dctnl

A;Molecule type: mRNA

A;Residues: 1-1281 <JAN>

A;Cross-references: UNIPROT:O08788; GB:U60312; MUID:g2104494; PIDN:AA857773.1; PID:921044

C;Comment: This protein is a member of the oligomeric dynactin complex that is required

A;Genetics: Dctnl

A;Map position: 6

Query Match 24.9%; Score 62.5; DB 2; Length 1281;  
Best Local Similarity 34.8%; Pred. No. 1.8e+02; Matches 16; Conservative 11; Mismatches 18; Indels 1; Gaps 1;

Qy 4 ETPOQKVQLRHEVQSLTTEVKIKTVKSSATEEKLTVLAKQL 49  
Db 319 ESLOQEVALKERVDPBLTDEILKAEIEEKGSQDGAAASVQL-KQL 363

RESULT 15

T3222 hypothetical protein T23B12.7 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T32222 R;Davidson, S.; Wohlmann, P.; Gillam, B.

submitted to the EMBL Data Library, September 1997

A;Description: The sequence of C. elegans cosmid T23B12.

A;Reference number: Z21137

A;Accession: T32222 A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-296 <DAV>

A;Cross-references: UNIPROT:O17002; EMBL:AF022382; PIDN:AAB69938.1; GSPDB:GN00023; CESP:

A;Experimental source: strain Bristol N2; clone T23P12

C;Genetics: CESP;r23B12.7

A;Gene: CESP;T23B12.7

A;Map position: 5

A;Intron: 67/3

Query Match 25.1%; Score 62; DB 2; Length 295;

Best Local Similarity 31.0%; Pred. No. 40; Matches 18; Conservative 12; Mismatches 12; Indels 16; Gaps 3;

Qy 3 KETPQQKYQRLHRLH---VQBLTEVEKIKTVKSSATEEKLTVLAKQL 47  
Db 132 KKTDPDNFK--EIEAARRQLEGEVNNERVKQATIMKTEREREKHOQSKPLKTRILLK 186

Search completed: November 3, 2005, 22:04:16  
Job time : 20.9091 secs

GenCore version 5.1.6  
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### OM protein - protein Search, using SW model

Run on: November 3, 2005, 21:37:29 ; Search time 91.4866 Seconds  
(without alignments)  
291.060 Million cell updates/sec

Title: 09782816-3-1-22

Perfect score: 251

Sequence: 1 GVKETPQQYQRLHLHEVQEL.....ESATEEKLTPVLLAKOAL 52

Scoring table: BLOSUM62

Gapop 10 0 , Gapext: 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03; \*

1: uniprot\_sprot; \*

2: uniprot\_trembl; \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query % Match Length	DB ID	Description
1	251	100.0	400	DCT2_HUMAN
2*	248	98.8	401	1 DCT2_MOUSE
3	248	98.8	402	2 Q6AYH5
4	220	87.6	403	2 O6IBR3
5	213	84.9	403	2 Q66J30
6	211	84.1	338	2 Q7ZKX2
7	177	70.5	402	2 Q7T3H1
8	177	70.5	405	2 Q61P53
9	76	30.3	402	2 Q9V4Y9
10	72.5	28.9	380	2 Q9V4Y9
11	71	28.3	800	2 Q6MPV7
12	71	28.3	813	2 Q7SH14
13	70	27.9	311	2 Q971V5
14	70	27.9	751	2 Q8MOK1
15	70	27.9	1087	2 Q86BSS
16	70	27.9	1124	2 Q8MQJB
17	70	27.9	2199	2 Q7UPU2
18	69.5	27.7	873	2 Q9SX56
19	69.5	27.7	919	2 Q95X55
20	68	27.1	1755	2 Q7RV31
21	68	27.1	1968	2 Q8X0C5
22	67.5	26.9	1868	2 Q6BNV2
23	67	26.7	455	2 Q7VVF1
24	67	26.7	639	2 Q6Z245
25	67	26.7	1795	2 Q9LCJ9
26	67	26.7	2478	2 Q9LCH2
27	67	26.7	2478	2 Q9LCH2
28	67	26.7	2481	2 Q9Q6
29	67	26.7	2481	2 Q7A4B1
30	66	26.3	393	2 Q49567
31	66	26.3	860	2 Q7QDQ9

### RESULTS

RESULT	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
RC	SEQUENCE FROM N.A.																														
RX	TISSUE=Placenta, Skin, and Uterus;																														
RA	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;																														
RA	Struberg R.L., Feingold L.H., Grouse L.H., Derge J.G.,																														
RA	Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,																														
RA	Altchul S.F., Zeeberg B.R., Buetow K.H., Schaefer C.F., Bhattacharyya S.P., Zeeberg B.R., Moore T., Max S.I., Wang J., Hsieh F., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,																														
RA	Diatchenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Faney J., Helton E., Kettemann M., Madan A., Rodriguez S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J.N., Schmitz J.J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,																														
RA	Scheich A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human cDNA sequences," Submitted (Nov-2002) to the EMBL/GenBank/DBJ databases.																														
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16893-16903 (2002).																														
RA	SEQUENCE OF 1-384 FROM N.A.																														
RA	Aunais J.-P., Yu-Lee L.-Y., "Human 50 kD dyneactin subunit, p50 dyneinin, isolated from HeLa cells," Submitted (Nov-2002) to the EMBL/GenBank/DBJ databases.																														
RA	[4]																														

SEQUENCE OF 1-384 FROM N.A.

Aunais J.-P., Yu-Lee L.-Y., "Human 50 kD dyneactin subunit, p50 dyneinin, isolated from HeLa cells," Submitted (Nov-2002) to the EMBL/GenBank/DBJ databases.

[4]

SEQUENCE OF 1-13.

084500 chlamydia t

Q8tbq8 homo sapien

074424 schizosaccharomyces pombe

07p225 anopheles gambiae

081j9 orza sativus

09bz3 homo sapien

09um0 homo sapien

092113 mus musculus

Q6dg9 brachydanio rerio

098i3 arabidopsis thaliana

07545 homo sapien

Q9gq1 drosophila melanogaster

09Y2K3 homo sapien

P51714 bacteriophage phiX174

RC TISSUE=Platelet;  
 RX MEDLINE=22380257; PubMed=12665801; DOI=10.1038/nbt810;  
 RA Gevertz K., Goethals M., Martens L., Van Damme J., Staes A.,  
 RA Thomas G.R., Vandekerckhove J., "Exploring proteomes and analyzing protein processing by mass  
 RT spectrometric identification of sorted N-terminal peptides.";  
 RL Biotechnol. 21:566-569(2003)  
 CC -!- FUNCTION: Modulates cytoplasmic dynein binding to an organelle,  
 CC and plays a role in prometaphase chromosome alignment and spindle  
 CC organization during mitosis. May play a role in synapse formation  
 CC during brain development.  
 CC -!- SUBUNIT: Subunit of dynein, a multiprotein complex associated  
 CC with dynein.  
 -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.  
 CC  
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 CC or send an email to license@isb-sib.ch).  
 CC  
 DR EMBL; US07033; AAC0423.1; -.  
 DR EMBL; BC000718; AAH0718.1; -.  
 DR EMBL; BC009468; AAH09468.1; -.  
 DR EMBL; BC014083; AAH14083.1; -.  
 DR Genew; HGNC:2112; DCTN2.  
 DR MIM; 60776; -.  
 GO; GO:0005813; C:centrosome; TAS.  
 GO; GO:0005869; C:dynein complex; TAS.  
 GO; GO:0008283; P:cell proliferation; TAS.  
 GO; GO:000767; P:mitosis; TAS.  
 DR InterPro; IPR06996; Dynamin.  
 DR Pfam; PF04912; Dynamin; 1.  
 DR Coiled coil; Cytoskeleton; Direct protein sequencing; Dynein;  
 KW Membrane; Microtubule; Motor protein.  
 FT INIT\_MET 0  
 FT DOMAIN 98 131 Coiled coil (Potential).  
 FT DOMAIN 213 243 Coiled coil (Potential).  
 FT DOMAIN 378 398 Coiled coil (Potential).  
 FT CONFLICT 34 34 A -> ARAQEL (in Ref. 1).  
 FT CONFLICT 35 35 E -> ELE (in Ref. 3).  
 FT CONFLICT 381 384 LATV -> PRHS (in Ref. 3).  
 SQ SEQUENCE 400 AA; 44099 MW; 0A95AE95C0BB270F CRC64;  
 Query Match 100.0%; Score 251; DB 1; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-17; 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 52; Conservative 0; MisMatched 0;  
 Qy 1 GVKERPPQKQYQRLHLHEQELTEVEKIKITWESATEEKUTPVLLAKQLAM 52  
 Db 93 GVKERTPQQKVQRLHLHEQELTEVEKIKITWESATEEKUTPVLLAKQLAM 144  
 RESULT 2  
 DCT2\_MOUSE STANDARD PRT 401 AA.  
 ID DCT2\_MOUSE  
 AC Q99KUB;  
 DT 09-FEB-2003 (Rel. 41, 'Created')  
 DT 05-JUL-2004 (Rel. 44, 'last sequence update')  
 DE Dynactin complex 50-kDa subunit (50 kDa dynein-associated polypeptide) (p50 dynamin) (DCDN-50) (Dynactin 2) (Growth cone membrane protein 23-48K) (GMP23-48K).  
 DE Name=Dctr2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Buteraria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.  
 RN [1] NCBI\_TaxID=10090;

RP SEQUENCE FROM N.A.  
 RX MEDLINE=22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RA Klausner R.D., Colling R.S., Wagner L., Sherman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Blat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bokse S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley P.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muñiz D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Farney J., Heiton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krywawych M.I., Skalska U., Smilus D.E.,  
 RA Schnurch A., Schein J.B., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16839-16803 (2002).  
 RN [2]  
 RP SEQUENCE OF 65-74; 77-91; 102-116; 156-170; 194-216 AND 309-320;  
 RP SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
 RN TISSUE=Brain;  
 RN INTERACTION WITH BICD2.  
 RX MEDLINE=2137052; PubMed=1483508; DOI=10.1093/emboj/20.15.4041;  
 RA Hoogenraad C.C., Akhmanova A., Howell S.A., Doortland B.R., Galjart N.,  
 RA de Zeeuw C.I., Willmesen R., Visser P., Grosfeld F., Galjart N.,  
 RT "Mammalian Golgi-associated Bicudal-D2 functions in the dynein-  
 RT dynein pathway by interacting with these complexes.";  
 RL EMBO J. 20:4041-4054 (2001).  
 CC -!- FUNCTION: Modulates cytoplasmic dynein binding to an organelle,  
 CC and plays a role in prometaphase chromosome alignment and spindle  
 CC organization during mitosis. May play a role in synapse formation  
 CC during brain development.  
 CC -!- SUBUNIT: Subunit of dynein, a multiprotein complex associated  
 CC with dynein (By similarity). Interacts with BICD2.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.  
 CC -!- DEVELOPMENTAL STAGE: Present at high levels in both cytoplasmic  
 CC and membrane-associated forms in neonates. Levels of membrane-  
 CC associated form are greatly reduced in the adult.  
 CC  
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 CC  
 DR EMBL; BC004613; AAH04613.1; -.  
 DR MGD; MGI:107733; Dctn2.  
 DR InterPro; IPR006996; Dynamin.  
 DR Pfam; PF04912; Dynamin; 1.  
 DR Coiled coil; Cytoskeleton; Direct protein sequencing; Dynein;  
 KW Membrane; Microtubule; Motor protein.  
 FT INIT\_MET 0  
 FT DOMAIN 98 131 By similarity.  
 FT DOMAIN 214 244 Coiled coil (Potential).  
 SQ SEQUENCE 401 AA; 43985 MW; 1535EABD5940EBC CRC64;  
 Query Match 98.8%; Score 248; DB 1; Length 401;  
 Best Local Similarity 98.1%; Pred. No. 9.4e-17; 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 51; Conservative 1; MisMatched 0;

RESULT 3

QY 1 GVKETPQQKQQLHEVQEVLTEVEKIKITVKESATEEKLTpvVLAQOAL 52  
ID 06AYH5 PRELIMINARY; PRT; 402 AA.  
AC Q6AYH5; DT 25-OCT-2004 (Tremblrel. 28, Created)  
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
DE Dynactin 2;  
GN Name=Dctn2;  
OS Rattus norvegicus (Rat).  
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Xenopus laevis; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;  
OC Xenopodinae; Xenopus.  
NCB!\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K.,  
RA Hopkins R.F., Jordan R., Moore T., Max S.I., Wang J.J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalon D.K., Munry D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,  
RA Blat N.K., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalon D.K., Munry D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Faley J., Heitton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalius D.E., Schnarch A., Schein J.B.,  
RA Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RA Director MGC Project; to the EMBL/GenBank/DBJ databases.  
RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; GO:0005869; AAH79042; AAH79042.1; -.  
DR GO; GO:0007017; P-microtubule-based process; IEA.  
DR Interpro; IPR006996; Dynamitin.  
DR Pfam; PF04912; Dynamitin; 1.  
SQ SEQUENCE 402 AA; 44148 MW; 55033553A4FB052 CRC64;

Query Match 98.8%; Score 248; DB 2; Length 402;  
Best Local Similarity 98.1%; Pred. No. 9.4e-17;  
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 4

QY 1 GVKETPQQKQQLHEVQEVLTEVEKIKITVKESATEEKLTpvVLAQOAL 52  
ID 06TRB3 PRELIMINARY; PRT; 403 AA.  
AC Q6TRB3; DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Dctn2-prov protein.  
GN Name=dctn2-prov;  
OS Xenopus laevis (African clawed frog).

RESULT 5

QY 1 GVKETPQQKQQLHEVQEVLTEVEKIKITVKESATEEKLTpvVLAQOAL 52  
ID 066U30 PRELIMINARY; PRT; 403 AA.  
AC Q66U30; DT 066U30; DT 25-OCT-2004 (Tremblrel. 28, Created)  
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
DE MGCB128 protein.  
GN Name=MGCB128;  
OS Xenopus laevis (African clawed frog).  
OC Xenopoda; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;  
OC Xenopodinae; Xenopus.

NCB!\_TaxID=8355;  
RN [1]



DR	GO; GO:0007017; P:microtubule-based process; IEA.
DR	InterPro; IPR06996; Dynamitin.
DR	Pfam; PF04912; Dynamitin_1.
SQ	SEQUENCE 402 AA; F229C467C630DCB9 CRC64;
Query	Match 70.5%; Score 177; DB 2; Length 402; Best Local Similarity 67.3%; Pred. No. 1. 2e-09; Matches 35; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
Db	96 GAKETRQQYKQLHBEVQELTTEVEKIKTTKESATEBEKLTPVLLAKOLANL 52
RESULT 8	
QT3HL	PRELIMINARY; PRT; 405 AA.
ID	0773HL
AC	Q7TAH1; PRELIMINARY; PRT; 405 AA.
DT	01-OCT-2003 (TREMBLrel. 25, last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE	Similar to dynactin_2 (P50).
GN	ORFNAMES-zgc:63867;
OS	Brychydario rario (Zebrafish) (Danio rerio).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
OX	NCBI_TaxID=7955;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;
RX	Medline=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Ringold E.A., Grouse L.H., Derge J.G.,
RA	Klaubner R.D., Collins F.S., Wagner L., Sheinman C.M., Schuler G.D.,
RA	Altshul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA	Raha S.S., Loqueland N.A., Peters K.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahey J., Helton E., Keeteman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grinwood J.M., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzewinski M.J., Skalska U., Smallius D.E., Scherich A., Schein J.B.,
RA	Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;
RX	Medline=22341132; PubMed=12454917; DOI=10.1002/dydy.10174;
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA	Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.", Dev. Dyn. 225:384-391 (2002).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;
RX	Klein S., Strausberg R.; "Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases. EMBL; BC053120; ARK53120; 1; -."
DR	ZFIN; ZDB-GENE-040426-1279; zgc:63867.
DR	GO; GO:0005869; C:dynamic complex; IEA.
DR	GO; GO:0007017; P:microtubule-based process; IEA.
DR	InterPro; IPR006936; Dynamitin.
DR	Pfam; PF04912; Dynamitin_1.
SQ	SEQUENCE 405 AA; 44625 MW; CA00047342500953 CRC64;
Query	Match 70.5%; Score 177; DB 2; Length 405; Best Local Similarity 67.3%; Pred. No. 1. 2e-09; Matches 35; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
Qy	1 GYKEPQQYKQLHBEVQELTTEVEKIKTTKESATEBEKLTPVLLAKOLANL 52
Db	96 GYKEPQQYKQLHBEVQELTTEVEKIKTTKESATEBEKLTPVLLAKOLANL 147
RESULT 9	
QT3HL	PRELIMINARY; PRT; 402 AA.
ID	061P53
AC	061P53; PRELIMINARY; PRT; 402 AA.
DT	05-JUN-2004 (TREMBLrel. 27, last sequence update)
DT	05-JUL-2004 (TREMBLrel. 27, last annotation update)
DE	MG78549 protein.
GN	Name=MG78549;
OS	Xenopus laevis (African clawed frog).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
OX	NCBI_TaxID=8355;
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RP	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;
RX	Medline=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA	Klaubner R.D., Collins F.S., Wagner L., Sheinman C.M., Schuler G.D.,
RA	Altshul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA	Raha S.S., Loqueland N.A., Peters K.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahey J., Helton E., Keeteman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grinwood J.M., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzewinski M.J., Skalska U., Smallius D.E., Scherich A., Schein J.B.,
RA	Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;
RX	Medline=22341132; PubMed=12454917; DOI=10.1002/dydy.10174;
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA	Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.", Dev. Dyn. 225:384-391 (2002).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;
RX	Klein S., Strausberg R.; "Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases. EMBL; BC02065; ARK2065; 1; -."
DR	GO; GO:0005874; C:microtubule; IEA.
DR	GO; GO:0000226; P:microtubule cytoskeleton organization and b... .; IEA.
DR	InterPro; IPR004435; Tekton.
DR	Pfam; PF03148; Tekton_1.
DR	PRINTS; PR00511; TEKTIN.
SQ	SEQUENCE 402 AA; 46535 MW; F173BC48FC0E798A CRC64;
Query	Match 30.3%; Score 76; DB 2; Length 402; Best Local Similarity 46.4%; Pred. No. 16; Matches 13; Conservative 10; Mismatches 5; Indels 0; Gaps 0;
Db	336 RLNEVQEITNTIRLRLTQSATEELK 363
RESULT 10	
QV4Y9	PRELIMINARY; PRT; 380 AA.

- AC Q9Y49; [4]  
 DT 01-MAY-2000 (TREMBrel. 13, Created)  
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)  
 DT 25-OCT-2004 (TREMBrel. 28, Last annotation update)  
 DE CG1269+PA (LDB7994P);  
 GN Name=Dmn; ORFNames=CG8669;  
 OS Drosophila melanogaster (Fruit fly).  
 BU Karuyota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydrioidea; Drosophilidae; Drosophila;  
 NCBI\_TaxID=7227;
- RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 Amatidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 Brandon R.C., Rogers Y.H., Blazej R.G., Channe M., Pfeiffer B.D.,  
 Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,  
 Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
 Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Boisshakov S.,  
 Botkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 Cherry J.M., Cawley S., Dahake C., Daverport L.B., Davies P.,  
 de Pablo B., Delcher A., Deng Z., Mayes A.D., Dew I., Dietz S.M.,  
 Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
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 Fosler C., Gabril A.E., Garg N.S., Gelbart W.M., Glaser K.,  
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegnami C.,  
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 Labko P., Lei Y., Levitt A.R., Li J., Li Z., Liang Y., Lin X.,  
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 Merkulov G., Milashina N.V., Mobarry C., Morris J., Mosbrefi A.,  
 Mount S.M., Moy M., Murphy L., Murphy L., Muzyk D.M., Nelson D.L.,  
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,  
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Purif V., Reese M.G.,  
 Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 Shue B.C., Sliden-Klamo I., Simpson M., Skupski M.P., Smith T.,  
 Spier E., Spradling A.C., Stadleton M., Strong R., Sun E.,  
 Svirkas R., Tector C., Turner R., Venter C., Wang A.H., Wang X.,  
 Wang Z.Y., Wasbarman D.A., Weinstock G.M., Weissenbach J.,  
 Williams S.M., Woodagek, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 Gibb R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287: 2185-2195 (2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426065; PubMed=12537568;  
 RA Celinker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
 Patel S., Adams M., Change M., Dugan S.P., Frise E., Hodgson A.,  
 George R.A., Hoskins R.A., Leverty T., Muzny D.M., Nelson C.R.,  
 Paclob J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 Svirkas R., Tabor B.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 Weinstock G., Scherer S.B., Myers E.W., Gibbs R.A., Rubin G.M.,  
 RT "Finishing a whole genome shotgun: Release 3 of the *Drosophila*  
 melanogaster euchromatic genome sequence.,";  
 RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirkas R.,  
 Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RT "Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 a genomics perspective.,";  
 RT Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
- RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hriadecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bernick B.P.,  
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
 RA Harris N.I., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 systematic review";  
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RG Flybase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DDJB databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RG Flybase;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DDJB databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkely;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Changie M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarini H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuovo J., Paclob J., Paraga V., Park S., Phouanenavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,  
 RA Submitted (OCT-2001) to the EMBL/GenBank/DDJB databases.  
 DR EMBL; AED0385; AFM5934.1; -.  
 DR EMBL; AY061092; AAL28640.1; -.  
 DR Intact; Q9V499; -.  
 DR FlyBase; FBgn0021825; Dman.  
 DR GO; GO:0005869; C:dynatin complex; IEA.  
 DR GO; GO:0007017; P:microtubule-based process; IEA.  
 DR InterPro; IPR06996; Dynamitin.  
 DR PFam; PF04912; Dynamitin\_1.  
 DR Sequence 380 AA; 41998 MW; CF7E1D3BFF5989C5 CRC64;  
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Query Match	28.9%; Score 72.5; DB 2; Length 380;
Best Local Similarity	48.7%; Pred. No. 34;
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Gap	94 GEKEIPVKQCKQLQEMMELNEVALLQD-RKVADBEK

  
 QY 39  
 DB 131
- RN RESULT 11  
 ID Q6MVPT  
 AC Q6MVPT  
 DT 05-JUL-2004 (TREMBrel. 27, Created)  
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)  
 DB Probable translation elongation factor EF-G, mitochondrial.  
 GN Name-B16018-090;  
 OS Neurospora crassa.  
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 RA Schultz E., Aign V., Hoheisel J., Brandt P., Partmann B., Holland R.,  
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA German Neurospora genome project;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX842625; CAE6249.1; -.  
 GO; GO:0005525; F:GTP binding; IEA.





DR InterPro; IPR002558; ILMEO.  
DR InterPro; IPR008943; PI\_bind\_N.  
DR Pfam; PF07651; ANTH; 1.  
DR Pfam; PF01608; I\_LWEO; 1.  
DR PRODOM; P001820; ILMEO; 1.  
DR PROSITE; PS50942; ENTH; 1.  
DR PROSITE; PS50945; I\_LWEO; 1.  
SQ SEQUENCE 1087 AA; \_L24298 MW; C83E709907DFEB8E8 CRC64;

Query Match 27.9%; Score 70; DB 2; Length 1087;  
Best local similarity 44.2%; Pred. No. 1.8e-02; Matches 19; Mismatches 9; Indels 4; Gaps 2;  
Matches 19; Conservative 9; Mismatches 11; Indels 4; Gaps 2;  
Matches 19; Conservative 9; Mismatches 11; Indels 4; Gaps 2;

QY 7 COKYORILHEVOELTVEEKKTTVKESEATEEKLTPLVLAQL 49  
DB 408 KQVNSQULLTEKLTNEISKIVNVEE---KEK-TNLILQKQI 446

Search completed: November 3, 2005, 22:03:04  
Job time : 94.4866 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 3, 2005, 21:51:39 ; Search time 26.6952 Seconds

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

**Database :**

Issued Patents AA:\*

- 1: /cgn2\_6/pctodata/1/iaa/5A\_COMB\_pep:\*
- 2: /cgn2\_6/pctodata/1/iaa/5B\_COMB\_pep:\*
- 3: /cgn2\_6/pctodata/1/iaa/6A\_COMB\_pep:\*
- 4: /cgn2\_6/pctodata/1/iaa/6B\_COMB\_pep:\*
- 5: /cgn2\_6/pctodata/1/iaa/PCTUS\_COMB\_pep:\*
- 6: /cgn2\_6/pctodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match %	Length	DB ID	Description
1	66	26.3	142	4	US-09-270-767-43370
2	64.5	26.9	144	4	US-09-270-767-43370
3	64	25.5	151	4	US-09-513-999C-7806
4	64	25.5	193	4	US-09-107-522A-5587
5	63	25.1	850	4	US-09-269-858A-8
6	63	25.1	851	4	US-09-623-326-43
7	62.5	24.9	1270	4	US-09-138-092-1321
8	61.5	30.9	4	US-09-248-796A-14974	
9	61	24.3	442	3	US-09-001-682-2
10	61	24.3	442	3	US-09-035-984-14
11	61	24.3	442	4	US-09-354A-14
12	61	24.3	442	4	US-09-443-940-14
13	61	24.3	442	4	US-09-563-110-5317
14	61	24.3	446	4	US-107-433-720
15	61	24.3	644	1	US-09-487-890A-6
16	61	24.3	644	2	US-08-978-435-6
17	61	24.3	644	2	US-08-337-483-6
18	61	24.3	644	2	US-08-448-377-6
19	61	24.3	644	3	US-08-474-671-6
20	61	24.3	644	3	US-08-537A-6
21	61	24.3	644	3	US-08-687-438-6
22	61	24.3	644	3	US-08-637-655-6
23	61	24.3	644	3	US-08-649-538-6
24	60.5	24.1	87	3	US-09-284-033-3
25	60.5	24.1	87	3	US-08-729-834B-3
26	60.5	24.1	1217	4	US-09-16-745-54
27	59.5	23.7	424	4	US-09-286-981B-14

**ALIGNMENTS**

RESULT 1  
US-09-270-767-43370

; Sequence 43370, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 43370

; LENGTH: 142

; TYPE: PRT

; ORGANISM: *Drosophila melanogaster*

US-09-270-767-43370

Query Match Best Local Similarity 26.3%; Score 66; DB 4; Length 142;

Matches 16; Conservative 50.0%; Pred. No. 1,6; Mismatches 3; Indels 13; Gaps 0; Gaps 0;

Ov Db

1 GVKETPQQYQRQLHVEQBLTTEVEKLTIVK 32  
111 GSKETPVQKQCLQIEMNELLNEVAALQVDRK 142

RESULT 2  
US-09-902-540-14908

; Sequence 14908, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wieand, Roger C.

; TITLE OF INVENTION: *Mycobacterium xanthus* Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-1019491B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; CURRENT PRIOR ART NUMBER: 60/217,883

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-10-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 14908

; LENGTH: 639

; TYPE: PRT

; ORGANISM: *Mycobacterium xanthus*

US-09-902-540-14908

Query Match 25.7%; Score 64.5; DB 4; Length 639;

Best Local Similarity 31.9%; Pred. No. 14; Matches 15; Conservative 11; Mismatches 12; Indels 9; Gaps 1; Software: ASCII

Query Match Sequence 5986, Application US/09513999C Current Application Data: Application Number: US/09/107,532A

Patent No. 6783951 Prior Application Data: Filing Date: 30-Jun-1998

Db GENERAL INFORMATION: Application Number: 60/085,98

Applicant: Dumas Milne Edwards, J.B. Attorney/Agent Information: Registration Number: 40,489

Applicant: Duclert, A. Name: Arinello, Pamela Denke

Title of Invention: Expressed Sequence Tags and Encoded Human Proteins. Reference/Docket Number: GTC-012

Patent No. 6783951 Telecommunication Information:

File Reference: 59 US2 REG Current Application Number: US/09/513,999C Telephone: (781)893-5007

Current Filing Date: 2000-02-24 Telefax: (781)893-8277

Prior Application Number: US 60/122,487 Information for Seq ID No: 5587:

Prior Filing Date: 1999-02-26 Sequence Characteristics:

Number of Seq ID Nos: 36681 Length: 193 amino acids

Software: Patent.pm Organism: Enterococcus faecium

Seq ID No: 7806 Type: amino acid

Length: 151 Topology: linear

Type: PRT Location: (B) LOCATION 1..193

Organism: Homo sapiens Molecule Type: protein

Feature: NAME/KEY: UNSURE Hypothetical: YES

Feature: NAME/KEY: SIGNAL Original Source:

Location: -25..-1 Feature: NAME/KEY: misc feature

Other Information: score 3.9 Location: (B) LOCATION 1..193

Feature: NAME/KEY: UNSURE Sequence Description: SEQ ID NO: 5587:

Location: 94 Other Information: Xaa=Lle or Lys or Asn or Arg or Ser or Thr

Feature: NAME/KEY: UNSURE

Location: 103 Other Information: Xaa=Glu or Iys

Location: 103 Other Information: Xaa=Glu or Iys

---

RESULT 4 US-09-513-999C-7806

Query Match 25.5%; Score 64; DB 4; Length 151; Best Local Similarity 40.5%; Pred. No. 3; Matches 17; Conservative 7; Mismatches 8; Indels 10; Gaps 1; Software: ASCII

Query Match 25.5%; Score 64; DB 4; Length 193; Best Local Similarity 40.5%; Pred. No. 3.9; Matches 15; Conservative 6; Mismatches 14; Indels 2; Gaps 1; Software: ASCII

Db GENERAL INFORMATION: Application Number: EP/96115877

Applicant: Lynn A Doucette-Stamm and David Bush Title of Invention: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

Applicant: Lynn A Doucette-Stamm and David Bush Title of Invention: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

Number of Sequences: 7310 Correspondence Address: ADDRESS: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street CITY: Waltham STATE: Massachusetts COUNTRY: USA ZIP: 02354

Computer Readable Form: Medium Type: CD-ROM ISO9660 Computer: PC Operating System: <Unknown>

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RESULT 5 US-09-269-858A-8

Query Match 25.5%; Score 64; DB 4; Length 193; Best Local Similarity 40.5%; Pred. No. 3.9; Matches 15; Conservative 6; Mismatches 14; Indels 2; Gaps 1; Software: ASCII

Query Match 25.5%; Score 64; DB 4; Length 193; Best Local Similarity 40.5%; Pred. No. 3.9; Matches 15; Conservative 6; Mismatches 14; Indels 2; Gaps 1; Software: ASCII

Db GENERAL INFORMATION: Application Number: EP/96115877

Applicant: Angerer, Bernhard Applicant: Ankenbauer, Waltraud

Applicant: Boeniringer, M. Applicant: Borch-Osmolovskaya, Elizaveta

Applicant: Markau, Ursula Applicant: Reiser, Astrid

Applicant: Schmitz-Aghaeian, Gudrun Applicant: Svetlicany, Vitaly

Applicant: Thermostable DNA Polymerase From Anaerocellum Thermophilum Title of Invention: Thermostable DNA Polymerase From Anaerocellum Thermophilum

File Reference: 4452 Current Application Number: US/09/269, 858A

Current Filing Date: 1999-06-10 Prior Application Number: PCT/EP97/05390

Prior Application Number: EP/96115877 Prior Filing Date: 1996-10-03

Prior Application Number: EP/96115877 Prior Filing Date: 1996-10-03

Number of Seq ID Nos: 8 Software: PatentIn Version 3.1

Seq ID No: 8 Length: 850

Type: PRT Organism: Abedus herberti

US-09-269-858A-8

Query Match 25.1%; Score 63; DB 4; Length 850; Best Local Similarity 30.9%; Pred. No. 28; Matches 17; Conservative 15; Mismatches 19; Indels 4; Gaps 2; Software: PatentIn Version 3.1



Query Match 24.3%; Score 61; DB 3; Length 442;  
 Best Local Similarity 33.3%; Pred. No. 23; Mismatches 24; Indels 6; Gaps 1;  
 Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

QY 2 VKEPQQKQYRQL-----LHEVQELTEVERKIKTVKESATEKLTTPVILAKQL 49  
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 Db 200 LKEQINSLYQHLLTVIADLHEKNEALIQLQEMKVFLRGASHELKTPLASLIKIL 253

RESULT 10  
 US-09-305-984-14  
 ; Sequence 14, Application US/09305984B  
 ; Patent No. 6331407  
 ; GENERAL INFORMATION:  
 ; APPLICANT: No. 6331407ak, Rodger  
 ; APPLICANT: Toumanen, Elaine  
 ; APPLICANT: Toumanen, Elaine, Blaine  
 ; TITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME  
 ; FILE REFERENCE: 1340-1-016N1  
 ; CURRENT APPLICATION NUMBER: US/09/305, 984B  
 ; CURRENT FILING DATE: 1999-05-05  
 ; EARLIER APPLICATION NUMBER: 60/084, 399  
 ; EARLIER FILING DATE: 1998-05-06  
 ; EARLIER APPLICATION NUMBER: 60/084, 399  
 ; EARLIER FILING DATE: 1998-05-06  
 ; EARLIER APPLICATION NUMBER: 09/305, 984  
 ; EARLIER FILING DATE: 1999-05-05  
 ; NUMBER OF SEQ ID NOS: 76  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 14  
 ; LENGTH: 442  
 ; TYPE: PRT  
 ; ORGANISM: Streptococcus pneumoniae  
 ; US-09-305-984-14

Query Match 24.3%; Score 61; DB 3; Length 442;  
 Best Local Similarity 33.3%; Pred. No. 23; Mismatches 24; Indels 6; Gaps 1;  
 Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

QY 2 VKEPQQKQYRQL-----LHEVQELTEVERKIKTVKESATEKLTTPVILAKQL 49  
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 Db 200 LKEQINSLYQHLLTVIADLHEKNEALIQLQEMKVFLRGASHELKTPLASLIKIL 253

RESULT 11  
 US-09-073-541A-14  
 ; Sequence 14, Application US/09073541A  
 ; Patent No. 6448224  
 ; GENERAL INFORMATION:  
 ; APPLICANT: No. 6448224ak, Rodger  
 ; APPLICANT: Toumanen, Elaine  
 ; APPLICANT: Toumanen, Elaine, Blaine  
 ; TITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME  
 ; FILE REFERENCE: 1340-1-016  
 ; CURRENT APPLICATION NUMBER: US/09/073, 541A  
 ; CURRENT FILING DATE: 1998-05-06  
 ; NUMBER OF SEQ ID NOS: 46  
 ; SEQ ID NO: 14  
 ; LENGTH: 442  
 ; TYPE: PRT  
 ; ORGANISM: Streptococcus pneumoniae  
 ; US-09-073-541A-14

Query Match 24.3%; Score 61; DB 4; Length 442;  
 Best Local Similarity 33.3%; Pred. No. 23; Mismatches 24; Indels 6; Gaps 1;  
 Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

QY 2 VKEPQQKQYRQL-----LHEVQELTEVERKIKTVKESATEKLTTPVILAKQL 49  
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 200 LKEQINSLYQHLLTVIADLHEKNEALIQLQEMKVFLRGASHELKTPLASLIKIL 253

RESULT 12  
 US-09-493-940-14  
 ; Sequence 14, Application US/09493940

Query Match 24.3%; Score 61; DB 4; Length 442;  
 Best Local Similarity 33.3%; Pred. No. 23; Mismatches 24; Indels 6; Gaps 1;  
 Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

QY 2 VKEPQQKQYRQL-----LHEVQELTEVERKIKTVKESATEKLTTPVILAKQL 49  
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 200 LKEQINSLYQHLLTVIADLHEKNEALIQLQEMKVFLRGASHELKTPLASLIKIL 253

RESULT 13  
 US-09-583-110-5317  
 ; Sequence 5317, Application US/09583110  
 ; Patent No. 6699703  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lynn Doucette-Stamm et al.  
 ; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
 ; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics  
 ; FILE REFERENCE: PAT10-07A  
 ; CURRENT APPLICATION NUMBER: US/09/583, 110  
 ; CURRENT FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/107, 433  
 ; PRIOR FILING DATE: 1998-06-30  
 ; PRIOR APPLICATION NUMBER: US 60/085, 131  
 ; PRIOR FILING DATE: 1998-05-12  
 ; PRIOR APPLICATION NUMBER: US 60/051, 553  
 ; PRIOR FILING DATE: 1997-07-02  
 ; NUMBER OF SEQ ID NOS: 5322  
 ; SEQ ID NO: 5317  
 ; LENGTH: 442  
 ; TYPE: PRT  
 ; ORGANISM: Streptococcus pneumoniae  
 ; US-09-583-110-5317

Query Match 24.3%; Score 61; DB 4; Length 442;  
 Best Local Similarity 33.3%; Pred. No. 23; Mismatches 24; Indels 6; Gaps 1;  
 Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

QY 2 VKEPQQKQYRQL-----LHEVQELTEVERKIKTVKESATEKLTTPVILAKQL 49  
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 200 LKEQINSLYQHLLTVIADLHEKNEALIQLQEMKVFLRGASHELKTPLASLIKIL 253

RESULT 14  
 US-09-107-433-3720  
 ; Sequence 3720, Application US/09107433  
 ; Patent No. 6800744  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lynn A Doucette-Stamm and David Bush  
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID  
 ; SEQUENCES RELATED TO STREPTOCOCUS PNEUMONIAE  
 ; NUMBER OF SEQUENCES: 5206  
 ; CORRESPONDENCE ADDRESS:



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OM protein - protein search, using sw model  
Run on: November 3, 2005, 21:53:15 ; Search time 93.7112 Seconds  
(without alignment)  
232.174 Million cell updates/sec

Title: 09792816-3-1-22  
Perfect score: 251  
Sequence: I GVKRTPQQKQYQRLHVEOVL. .... ESATEBKLTPTVLLAKOAL 52

Scoring table: BLOSUM62  
Gapext 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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17: /cgn2\_6/podata/1/pubpaa/US10E\_PUBCOMB.pep:  
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21: /cgn2\_6/podata/1/pubpaa/US60\_NEW\_PUB.pep:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	% Query Match Length	DB ID	Description	
1	251	100.0	401	16 US-10-408-765A-1369	Sequence 1369, App
2	251	100.0	406	10 US-09-782-816A-53	Sequence 53, App
3	251	100.0	465	9 US-09-925-298-676	Sequence 676, App
4	251	100.0	465	14 US-10-102-805-676	Sequence 676, App
5	248	98.8	183	10 US-09-782-816A-54	Sequence 54, App
6	248	98.8	224	16 US-10-125-115-315831	Sequence 315831, App
7	246	98.0	52	10 US-09-821-816A-51	Sequence 51, App
8	231	92.0	134	14 US-10-106-698-6730	Sequence 6730, App
9	113	45.0	22	10 US-09-782-816A-3	Sequence 3, App
10	107	42.6	21	10 US-09-782-816A-4	Sequence 4, App
11	103	41.0	20	10 US-09-782-816A-5	Sequence 5, App

10: /cgn2\_5/\_ptodata1/pupaa/us09\_pubcomb.pep:\*
 11: /cgn2\_6/\_ptodata1/pupaa/us09c\_pubcomb.pep:\*
 12: /cgn2\_6/\_ptodata1/pupaa/us09\_new\_pub.pep:\*
 13: /cgn2\_6/\_ptodata1/pupaa/us10\_pubcomb.pep:\*
 14: /cgn2\_6/\_ptodata1/pupaa/us10b\_pubcomb.pep:\*
 15: /cgn2\_6/\_ptodata1/pupaa/us10c\_pubcomb.pep:\*
 16: /cgn2\_6/\_ptodata1/pupaa/us10d\_pubcomb.pep:\*
 17: /cgn2\_6/\_ptodata1/pupaa/us10e\_pubcomb.pep:\*
 18: /cgn2\_6/\_ptodata1/pupaa/us10\_new\_pub.pep:\*
 19: /cgn2\_6/\_ptodata1/pupaa/us11a\_pubcomb.pep:\*
 20: /cgn2\_6/\_ptodata1/pupaa/us11\_new\_pub.pep:\*
 21: /cgn2\_6/\_ptodata1/pupaa/us60\_new\_pub.pep:\*
 22: /cgn2\_6/\_ptodata1/pupaa/us60\_pubcomb.pep:\*

**Pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score or the result being printed, and is derived by analysis of the total score distribution.

**RESULT**: 1  
 US-10-408-765A-1369  
 Sequence 1369, Application US/10408765A  
 Publication No. US20040101874AI  
 GENERAL INFORMATION:  
 APPLICANT: Ghosh, Soumitra S.  
 APPLICANT: Farly, Boin D.  
 APPLICANT: Zhang, Bing  
 APPLICANT: Gibson, Bradford W.  
 APPLICANT: Taylor, Steven W.  
 APPLICANT: Glenn, Gary M.  
 APPLICANT: Watnick, Dale E.  
 TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
 TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
 FILE REFERENCE: 660088.465  
 CURRENT APPLICATION NUMBER: US/10/408,765A  
 CURRENT FILING DATE: 2003-04-04

## ALIGNMENTS

RESULT 2  
US-09-782-816A-53  
; Sequence 53, Application US/09782816A  
; Publication No. US20030032771A1  
; GENERAL INFORMATION:  
; APPLICANT: Sharp, David J.  
; APPLICANT: Rogers, Gregory C.  
; APPLICANT: Scholey, Jonathon M.  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR PROLIFERATION  
; FILE REFERENCE: UC069\_001A  
; CURRENT APPLICATION NUMBER: US/09/782,816A  
; CURRENT FILING DATE: 2001-02-14  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 406  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-782-816A-53

Query Match 100.0%; Score 251; DB 10; Length 406;  
Best Local Similarity 100.0%; Pred. No. 1.6e-19;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKETPQQKVRQLHEVQEVLTEVEKIKTVKESATEEKUTPVLLAKQAL 52  
Db 99 GVKETPQQKVRQLHEVQEVLTEVEKIKTVKESATEEKUTPVLLAKQAL 150

RESULT 3  
US-09-925-298-676  
; Sequence 676, Application US/09925298  
; Publication No. US20030039764A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA103  
; CURRENT APPLICATION NUMBER: US/09/925,298  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05881  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 846  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 676  
; LENGTH: 465  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: SITE  
; NAME/KEY: SITE  
; LOCATION: (5)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: SITE  
LOCATION: (6)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: SITE  
LOCATION: (16)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-102-806-676

Query Match 100.0%; Score 251; DB 14; Length 465;  
Best Local Similarity 100.0%; Pred. No. 1.8e-19;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKETPQQKVRQLHEVQEVLTEVEKIKTVKESATEEKUTPVLLAKQAL 52  
Db 158 GVKETPQQKVRQLHEVQEVLTEVEKIKTVKESATEEKUTPVLLAKQAL 209

RESULT 5  
US-09-782-816A-54  
; Sequence 54, Application US/09782816A  
; Publication No. US20030032771A1  
; GENERAL INFORMATION:  
; APPLICANT: Sharp, David J.  
; APPLICANT: Rogers, Gregory C.  
; APPLICANT: Scholey, Jonathon M.  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR PROLIFERATION  
; FILE REFERENCE: UC069\_001A  
; CURRENT APPLICATION NUMBER: US/09/782,816A  
; CURRENT FILING DATE: 2001-02-14  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 54  
; LENGTH: 183  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-782-816A-54

Query Match 98.8%; Score 248; DB 10; Length 183;  
Best Local Similarity 98.1%; Pred. No. 1.3e-19;  
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKETPQQKVRQLHEVQEVLTEVEKIKTVKESATEEKUTPVLLAKQAL 52  
Db 94 GVKETPQQKVRQLHEVQEVLTEVEKIKTVKESATEEKUTPVLLAKQAL 145

RESULT 6  
US-10-425-115-315831

RESULT 4  
US-10-102-806-676

Sequence 315831, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovacic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(5322)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 315831  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_51109C.1.pep  
; US-10-425-115-315831

RESULT 7  
US-09-782-816A-51  
; Sequence 51, Application US/09782816A  
; Publication No. US20030032771A1  
; GENERAL INFORMATION:  
; APPLICANT: Sharp, David J.  
; APPLICANT: Rogers, Gregory C.  
; APPLICANT: Scholey, Jonathon M.  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR  
; TITLE OF INVENTION: PROLIFERATION  
; FILE REFERENCE: UC009\_001A  
; CURRENT APPLICATION NUMBER: US/09/782,816A  
; CURRENT FILING DATE: 2001-02-14  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 51  
; LENGTH: 52  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 44  
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus  
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus  
; OTHER INFORMATION: musculus.  
; OTHER INFORMATION: musculus.  
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus  
; OTHER INFORMATION: musculus.  
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; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus  
; OTHER INFORMATION: musculus.  
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus  
; OTHER INFORMATION: musculus.

Query Match 98.0%; Score 246; DB 10; Length 52;  
Best Local Similarity 98.1%; Pred. No. 5e-20; Mismatches 1; Indels 0; Gaps 0;  
Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVKETPQQKQYQLHEVOELTTEVEKIKITVKESATEEKLTPTVILAKOAL 52  
Db 1 GVKETPQQKQYQLHEVOELTTEVEKIKITVKESATEEKLTPTVILAKOAL 52

RESULT 8  
US-10-106-698-6730  
; Sequence 6730, Application US/10106698  
; Publication No. US20030105690A1  
; GENERAL INFORMATION:  
; APPLICANT: Sharp, David J.  
; APPLICANT: Rogers, Gregory C.  
; APPLICANT: Scholey, Jonathon M.  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides

Query Match 98.0%; Score 246; DB 10; Length 52;  
Best Local Similarity 98.1%; Pred. No. 5e-20; Mismatches 1; Indels 0; Gaps 0;  
Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVKETPQQKQYQLHEVOELTTEVEKIKITVKESATEEKLTPTVILAKOAL 52  
Db 1 GVKETPQQKQYQLHEVOELTTEVEKIKITVKESATEEKLTPTVILAKOAL 52

RESULT 9  
US-09-782-816A-3  
; Sequence 3, Application US/09782816A  
; Publication No. US20030032771A1  
; GENERAL INFORMATION:  
; APPLICANT: Sharp, David J.  
; APPLICANT: Rogers, Gregory C.  
; APPLICANT: Scholey, Jonathon M.  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR  
; TITLE OF INVENTION: PROLIFERATION  
; FILE REFERENCE: UC009\_001A  
; CURRENT APPLICATION NUMBER: US/09/782,816A  
; CURRENT FILING DATE: 2001-02-14  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 44  
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus  
; OTHER INFORMATION: musculus.  
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus  
; OTHER INFORMATION: musculus.  
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus  
; OTHER INFORMATION: musculus.

Query Match 92.0%; Score 231; DB 14; Length 134;  
Best Local Similarity 100.0%; Pred. No. 7.1e-18; Mismatches 6; Indels 0; Gaps 0;  
Matches 48; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 5 TPQQKQYQLHEVOELTTEVEKIKITVKESATEEKLTPTVILAKOAL 52  
Db 1 TPQQKQYQLHEVOELTTEVEKIKITVKESATEEKLTPTVILAKOAL 48

RESULT 10  
US-09-782-816A-4  
; Sequence 4, Application US/09782816A  
; Publication No. US20030032771A1  
; GENERAL INFORMATION:  
; APPLICANT: Sharp, David J.  
; APPLICANT: Rogers, Gregory C.  
; APPLICANT: Scholey, Jonathon M.  
; APPLICANT: Peptide Inhibitors Of Cellular  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR  
; TITLE OF INVENTION: PROLIFERATION

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FILE REFERENCE: UC069_001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 4
LENGTH: 21
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
OTHER INFORMATION: musculus.
US-09-782-816A-4

Query Match
Best Local Similarity 42.6%; Score 107; DB 10; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 VKEPQQKQQLHEVQELTT 21

RESULT 11
US-09-782-816A-5
; Sequence 5, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathon M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR PROLIFERATION
; FILE REFERENCE: UC069_001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; LENGTH: 20
; SEQ ID NO: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
; OTHER INFORMATION: musculus.
US-09-782-816A-5

Query Match
Best Local Similarity 100.0%; Score 103; DB 10; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 VKEPQQKQQLHEVQELTT 21

RESULT 12
US-09-782-816A-1
; Sequence 1, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathon M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR PROLIFERATION
; FILE REFERENCE: UC069_001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
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; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
; OTHER INFORMATION: musculus.
US-09-782-816A-4

Query Match
Best Local Similarity 41.0%; Score 103; DB 10; Length 23;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 EVEKIKTTKESATEEKCPVXL 23

RESULT 13
US-09-782-816A-6
; Sequence 6, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathon M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR PROLIFERATION
; FILE REFERENCE: UC069_001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; LENGTH: 19
; SEQ ID NO: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
; OTHER INFORMATION: musculus.
US-09-782-816A-6

Query Match
Best Local Similarity 39.0%; Score 98; DB 10; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 ETPQQKQQLHEVQELTT 19

RESULT 14
US-09-782-816A-7
; Sequence 7, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathon M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR PROLIFERATION
; FILE REFERENCE: UC069_001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; LENGTH: 18
; SEQ ID NO: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:

```

; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus  
; OTHER INFORMATION: musculus.  
US-09-782-816A-7

Query Match 37.1%; Score 93; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.0014; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 18; Conservative 0;

Qy	5	PQQKXQRLIHEVQELTT	22
Db	1	TpQKXQRLIHEVQELTT	18

RESULT 15  
US-09-782-816A-8  
; Sequence 8, Application US/09782816A  
; Publication No. US20030032771A1  
; GENERAL INFORMATION:  
; APPLICANT: Sharp, David J.  
; APPLICANT: Rogers, Gregory C.  
; APPLICANT: Scholey, Jonathon M.  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR  
; PROLIFERATION  
; FILE REFERENCE: UC009.001A  
; CURRENT APPLICATION NUMBER: US/09/782,816A  
; CURRENT FILING DATE: 2001-02-14  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSBQ for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus  
; OTHER INFORMATION: musculus.  
US-09-782-816A-8

Query Match 35.1%; Score 88; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.0048; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 17; Conservative 0;

Qy	6	PQQKXQRLIHEVQELTT	22
Db	1	PQQKXQRLIHEVQELTT	17

Search completed: November 3, 2005, 22:11:40  
Job time : 94.712 secs

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